```
Command line parameters:

-MODEL-frame-_n2p.model -DEW=xlh
-O--Cgn2_1/USPTO_Spool/US09998982/runat_27012003_073716_19567/app_query.fasta_1.967
-OB-SPTREMBL_21 -OFMT=-fastan -SUFFIX=n2p.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALION=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTEMT=pto -NORM-ext -HEAPSTE=500 -MINLEN=0 -MAXEN=200000000
-USER=US09598982_@CGN_1_1_80_erunat_27012003_073716_19567 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                             Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BC
                             Score
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length: 2000000000
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Match Length DB
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sp_phage:*
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sp_rvirus:*
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sp_archeap:*
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sp_virus:*
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Ygapext
Fgapext
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6418.680 Million cell updates/sec
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  Q96rz6 homo sapien
                        Description
RESULT 1
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0917V4
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Q95ME7
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Q9BYE2
Q9DBI0
L Q9DY47
L Q9DAT3
O18783
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Q924N9
Q96L36
Q9RNA6
Q9PVX7
Q91XC4
3 Q9DGR3
1 Q9DGR3
1 Q9QYZ9
Q9QYZ9
Q9QYZ9
Q9QYZ9
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Q97SM1
Q29464
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Q90Q18
Q90Q18
Q8TD16
Q8SQ44
Q8SQ44
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O97506 sus scrofa
O9w7q5 paralichthy
Q9d413 mus musculu
O96899 scolopendra
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Q9pvx7 xenopus lae
Q91xc4 mus musculu
Q9dgr3 xenopus lae
Q9dyr9 mus musculu
Q99144 mus musculu
Q99144 mus musculu
Q88781 rattus ratt
Q8vde0 mus musculu
Q42272 xenopus lae
Q8vif2 mus musculu
Q4272 xenopus lae
Q8vif2 mus musculu
Q95me7 oryctolagus
Q9bye1 homo sapien
Q9bye2 homo sapien
Q9bye1 mus musculu
Q91x47 mus musculu
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Q91x48 masropus eu
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Ogsq44 sus scrofa
Oggms4 mus musculu
     Q9w7q1 paralichthy
Q15146 homo sapien
Q8vca5 mus musculu
046506 papio hamad
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Q917v4 drosophila
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Q924n9 mus musculu
Q96136 homo sapien
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Q91674 xenopus lae
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## ALIGNMENTS

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096RZ6

096RZ6;

01-DEC-2001 (TrembLrel. 1

01-DEC-2001 (TrembLrel. 1

01-JUN 2002 (TrembLrel. 2
                                "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
EMBL, AE006466; AAK61271.1;
                                                                                                                                                                                                                                                Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                   MEDLINE=21096910; PubMed=11157797; Daniels R.J., Peden J.F., Lloyd C., Tufarelli C., Kearney L., Buckle V.
                          MEROPS; S01.242;
                                                                                                                                                                                              SEQUENCE FROM N.A.
      InterPro;
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IPR001254; Ser_protease_Try.
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19,
21,
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Last annotation update)
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A., Flint
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Score:
RESULT 2
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ID Q921
AC Q921
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pROSITE; PS50240; TRYPSIN_DOM;
PROSITE: PS00134; TRYPSIN_IS;
PROSITE; PS00135; TRYPSIN_SER;
Q921N4;
Q921N4;
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SEQUENCE
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ValProLysLysPro 275
                                                       AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG
                                                                                                                TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
                                                                                                                                   {\tt ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla}
                                                                                                                                                                   CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
                                                                                                           CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
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275 AA;
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      PRELIMINARY;
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97.96%
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Matches:
Conservative:
Mismatches:
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Mammalia; Eutheria
NCBI_TaxID=10090;
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001254; Ser_protease_Try.
pfam; pF00089; trypsin; 1.
proSITE; pS50240; TRYPSIN_HIS; UNKNOWN_1.
pROSITE; pS00134; TRYPSIN_HIS; UNKNOWN_1.
pROSITE; pS00135; TRYPSIN_SER; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
SEQUENCE 273 AA; 30332 MW; 5141747651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCPT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL; BC011328; AAH11328.1;
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                                                          ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC:::||||||||:::|||
                                                                                                                                                                                                               ProProAlaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsn
               CGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGC
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3.82e-72
1049.00
81.67%
74.90%
71.95%
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Rodentia;
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Sciurognathi; Muridae;
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Indels:
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                                                                                                                                                                                                                                  Local
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PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                              "Sequence, structure and pathology of the fully annotated mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).
EMBL; AE006466; AAK61270.1; -.
MEROPS; S01.027; -.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=21096910; PubMed=11157797;

Daniels R.J., Peden J.F., Lloyd C., Horsley
Tufarelli C., Kearney L., Buckle V.J., Dogge
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96RZ7;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG
                                  ATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC
                                                                                                                        CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
                                                                                                              ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu
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Matches:
Conservative:
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Doggett N.A.,
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RESULT
Q9XSM1
US-09-598-982-20 (1-771) x Q9XSM1 (1-273)
                                                                                                   Query Match:
                                        Best Local Similarity:
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01-NOV-1999 (TrEMBLrel. 12, C)
01-NOV-1999 (TrEMBLrel. 12, L
01-JUN-2002 (TrEMBLrel. 21, L
Tryptase (EC 3.4.21.59).
                                                                                                                                                                                                                                                       Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D. Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.; "cDNA sequence of two sheep mast cell tryptases and the expression of tryptase and sheep mast cell proteinase-1 dermis and gastrointestinal tract."; Clin. Exp. Allergy 30.818-883(2000).
                                                                                                                                                                                                                                                                                                                                                        SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                    Hydrolase;
                                                                                                                                                                   InterPro; IPR001254; Ser_protease_Try. Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN.
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HSSP; P20231; 1AAO.
MEROPS; S01.118; -.
                                                                     No.:
                                                                                                 SEQUENCE
                                                                                                            CHAIN
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InterPro; IPR001254;
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TRYPSIN FAMILY.
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
Tryptase (EC 3.4.21.59) (
TISSUE-LIVER CAPSULE;

MEDITINE-96203914; PubMed-8620861;

Pallaoro M., Gambacurta A., Fiorucci L., Mignogna G., Barra Ascoli F.;

"CDNA cloning and primary structure of tryptase from bovine and evidence of the expression of bovine pancreatic trypsin mRNA in the same cells.";

Eur. J. Biochem. 237:100-105(1996).
                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Ru
                                                                                                       Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                     SEQUENCE FROM N.A.
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Ruminantia; Pecora; Bovoidea
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InterPro; IPR001254; Ser_proteas
Pram; Pr00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1
PROSITE; PS00134; TRYPSIN_HIS; U
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SEQUENCE 237 AA; 26550 M
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RESULT 6
Q96R
AC Q96R
AC Q96R
DT Q1-D
DT Q1-M
DT Q1-M
OS Homo
OC Euka
GN MMCP
OS Homo
OX NCB11
RN [1]
RN [1]
RN [1]
RA Tifa
RA Higa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96RZ5 PRELIMINARY; PRT; 242 AA.
Q96RZ5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative mast cell MMCP-7-like II tryptase (MMCP-7-like-2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
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MEDLINE=21096910; PubMed=11157797;

Daniels R.J., Peden J.F., Lloyd C., Horsley
Tufarelli C., Kearney L., Buckle V.J., Dogge
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CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
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                                                                                                                CCGGGGATGCCGTGCTGGCTGGCTGGCGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
                                                                                                                                                                                                        GTGAAGGTCTCCAGCGTCCACACGGTCACACGCTGCCCCCTGCCTCAGAGACCTTCCCC
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                                                                                        {\tt ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsnValHisLeuPro}
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84.39%
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Gaps:
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Doggett N.A.,
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A., Flint
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Q9UQI8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mast cell mMCP-7-like I protein (Fragment).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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NON_TER 166 166
SEQUENCE 166 AA; 18433 M
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SMART; SM00020; TRYP_SPC; 1.
PROSITE: PS50240; TRYPSIN_DOM:
PROSITE: PS00134; TRYPSIN_HIS;
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SIMILARITY: BELONGS
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{\tt GluTyrHisThrGlyLeuHisThrGlyHisSerPheGlnIleValArgAspAspMetLeu}
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2; CHYMOTRYPSIN
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699.00
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91.18%
47.94%
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Mismatches:
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Homo sapiens (Human).
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                               131
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 112
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130 A
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651.50
87.05%
84.17%
44.68%
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14765 MW;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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08SQ44;

01SQ44;

01-JUN-2002 (TrEMBLrel. 21,

01-JUN-2002 (TrEMBLrel. 21,

01-JUN-2002 (TrEMBLrel. 21,
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                        GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG
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TyrargValLysLeuGlyArgTrpMetHisHisCysGlyGlySerLeuValHisProGln
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Enzyme from Porcine
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Query Match:
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O1-JUN-2001 (TrEMBLrel. 17, Create

O1-OCT-2001 (TrEMBLrel. 18, Last;

O1-JUN-2002 (TrEMBLrel. 21, Last;

O1-JUN-2003 (TrEMBLrel. 21, Last;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen Q.-X., Wang J., Huang Z.-P.;
"Identification of endometrial fautimplantation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21361749; PubMed=11467974; O'Sullivan C.M., Liu S.Y., Rancourt "Regulation of the strypsin-related endometrial gland epithelium during Reproduction 122:235-244(2001).
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99MS4
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                              Hydrolase;
SEQUENCE
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EMBL; AF442819; AAL38005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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Sciurognathi;
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Q96RZ8;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                SEQUENCE FROM N.A.

MEDLINE-21096910; PubMed-11157797;

Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Cla

Tufarelli C., Kearney L., Buckle V.J., Doggett N.A.,
           MEROPS; S01.028;
InterPro; IPR0012
                                 "Sequence, structure and pathology Mb of the short arm of human chrom Hum. Mol. Genet. 10:339-352(2001).
EMBL; AE006466; AAX61269.1; -.
                                                                                       Higgs D.R.;
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                   TRPA.
                                                                                                                                                                                                                               HS transmembrane
                                                                                                                                                               NCBI_TaxID=9606;
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PF00089; trypsin;
           IPR001254;
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                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Ser_protease_Try
in; 1.
                                                                          pathology of the
                                                                                                                                                                                                                            gene name
                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
gene name TMT, AF175522_1.
                                                                                                                                                                                                                                                                    Created)
                                                              chromosome
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Catarrhini; Hominidae
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Percent Similarity:
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Q924N9;
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01-DEC-2001
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SEQUENCE
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                                                                                                                                                                                                                                                                                                               {\tt ProLeuProProTyrSerLeuArgGluValLysValSerValValAspThrGluThr}
                                                                                                                                                                                                                                                                                                                                                            AspPheCysProGlyIleArgCysTrpValThrGlyTrpGlyTyrThrArgGluGlyGlu
                                                                                ArgArgHisIle
                                                                                                     CACCACTATGTC 741
                                                                                                                                       TGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATC
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                                                                                                                                                                                                                                                                                          TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGGACGTCCGCCATCGTCCGTGAC
                                                                                                                                                                                                                                                                                                                                      CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT
                                                                                                                           {\tt CysGlyArgProAsnArgProGlyValTyrThrArgValProAlaTyrValAsnTrpIle}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S50240; TRKPSIN_DOM; 1.
S00134; TRKPSIN_H1S; UNKNOWN_1.
Serine protease; Transmembrane.
321 AA; 33829 MW; FFF5089EDC4FC73D
 (TrEMBLrel.
                                   PRELIMINARY;
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589.50
61.89%
48.36%
40.43%
19,
19,
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Last sequence
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.

PROSITE; PS50240; TRYPSIN_HIS; U
PROSITE; PS00134; TRYPSIN_SER; U
PROSITE; PS00135; TRYPSIN_SER; U
Hydrolase; Serine protease.
SEQUENCE 274 AA; 30628 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; ROSI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21319572; PubMed=11425330;
O'Sullivan C.M., Rancourt S.L., Liu
"A novel murine tryptase involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Las Implantation serine proteinase. ISP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.314; -. MGD; MGI:2149951; Isp1 InterPro; IPR001254; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reproduction 122:61-71(2001).
EMBL; AF184895; AAK84171.1; -
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                                                                                                                                                                                                                                                                                         GTGCAACTGCGGGAGCACCTCTACTACCAGGACCAGCTGCTGCTGCCGGTCAGCAGGATC
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TyrSerTyrGluValAsnSerTrpValHiSIleCysGlyGlySerIleIleHisProGln
                                                                                                                                                                                                                                                                                                                                                                                                       CACGGC-----CCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG
 GACATGCTGTGTGCCGGGAACACCCGGAGGGAACTCATGCCAGGGCGACTCCGGAGGGCCC
                                                                                      CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT
                                                                                                                         {\tt ThrPheAspSerThrAspGlnCysTrpLeuValGlyTrpGlyAsnLeuLeuGlnArgValue} \\
                                                                                                                                        ThrAlaLeuLeuValThrSerThrAsnValSerProValSerLeuProLysAspSerSer
                                                                                                                                                                                                    GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACCCTGCCCTGCCTCAGAG
                                                                                                                                                                                                                            {\tt IleIleHisProAspTyrAsnAspValSerLysArgPheAspLeuAlaLeuMetGlnLeu}
                       CysLysArgAlaTyrArgLysLysSerSerAspGluH1sLysAlaValAlaIlePheAsp
                                                 TGTGACGCAAAATACCACCTTGGCGCCCTACACGGGAGACGACGTCCGCATCGTCCGTGAC
                                                                          ProLeuGlnProProTyrGlnLeuHisGluValLysIleProIleGlnAspAsnLysSer
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60.25%
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Sciurognathi;
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Q96L36;
Q96L36;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Delta I tryptase (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hunt J.E., Wang H.W., Thomas P.S., McNeil P.; "Cloning and characterization of novel human tryptase cDNAs."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY055427; AAL17874.1; -. InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
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SEQUENCE 331 AA; 3
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US-09-598-982-20 (1-771) x Q8R1A6
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Q8R1A6;
O1-JUN-2002 (TrEMBLrel. 21, C
O1-JUN-2002 (TrEMBLrel. 21, I
O1-JUN-2002 (TrEMBLrel. 21, I
RIKEN CDNA 2010001P08 gene.
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{\tt ValIleLeuGluGlyMetLeuCysAlaGlyPheGlnGlnGlyLysLysAspAlaCysAsn}
                                                      ATCGTCCGTGACGACATGCTGTGTGCCGGG-----AACACCCCGGAGGGACTCATGCCAG
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                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS50135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9PVX7; PRELIMINARY; PRT; 389 AA.
O9PVX7; 01-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The expression control of xepsin by non-axial and planar posteriorizing signals in xenopus epidermis."; submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN TRYPSIN FAMILY.
EMBL; ABOLB694; BAA84941.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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ThrValTyrLeuGlyAlaTyrGlnLeuSerAlaProAspAsn---SerThrValSerArg
                                                      |||||||:::||||||||| ||||:::
|SerTrpValMetThrAlaAlaHisCysIle--
                                                                                  CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC
                                                                                                                                                                  CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCCTGGCAGGTG 66
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                          AGGGTGCAACTGCGGGAGCAGCCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG
                                                                                                            SerLeuSerTyrLysSerAsp-----SerIleCysGlyGlySerLeuLeuThrAsp
                                                                                                                                         AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCC
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                                                                                                                                                                                                                                                                                                                                                                       Protease; 389 AA; 4
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543.00
57.14%
42.86%
37.24%
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42375 MW; B31FB4A2F5D1F6E3
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Matches:
Conservative:
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Indels:
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ia; Pipoidea; Pipidae;
                                                      -AspSerLeuAspValSerTyrTyr
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                                                                                                                               GlnGlyAspSerGlyGlyProLeuValCysAsnValAsnAsnValTrpLeuGlnLeuGly
                                 ACCTACTACTTGGACTGGATCCACCACTATGTCCCC 744
                                                                                                GTGGTCAGCTGGGGGGGGGGTGTGCCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTC
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GlnTyrTyrGlnAspTrpLeuLysThrAsnValPro
                                                               SerPheIleGlnGluAspMetValCysAlaGlyTyrLysGluGlyArgIleAspAlaCys
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Search completed: January 31, 2003, 06:58:26 Job time: 63.5 secs



Run OM nucleic - protein search, using frame\_plus\_n2p model on : January 31, 2003, 05:25:33 ; Search time 17.5 Seconds (without alignments) 3654.657 Million cell updates/sec GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

Title: Perfect score: Sequence: US-09-598-982-20 1458 gggcccctcgagaaaagaat.....cgtgaagcggccgccgtcgt 771

Scoring table:

BLOSUM62
X9apop 10.0 , X9apext
Y9apop 10.0 , Y9apext
F9apop 6.0 , F9apext
F9apop 6.0 , Delext 0.5 0.5 7.0 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL-frame+\_n2p.model -DEV=xlh
-Q-Cgn2\_1/USPTO\_spool/US09598982/runat\_27012003\_073715\_19534/app\_guery.fasta\_1.967
-Q-Cgn2\_1/USPTO\_spool/US09598982/runat\_27012003\_073715\_19534/app\_guery.fasta\_1.967
-DB=SwissProt\_40 -QFMT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR\_SCORR-pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000
-USER=US09598982\_eCGN\_1\_1\_6\_erunat\_27012003\_073715\_19534 -NCPU=6 -ICPU=3
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Ľα	17	16	15	14	13	12	11	10	9	· œ	7	10	ۍ .	4	u	٠ ٨:	سر ،	No.	Result
526	529	563.5	593.5	608.5	684.5	988	1006	1030	1039	1055	1057	1075	1077	1092	1282	1363	1368	Score	
36.1	36.3	38.6	40.7	41.7	46.9	67.8	69.0	70.6	71.3	72.4	72.5	73.7	73.9	74.9	87.9	93.5	93.8	Match 1	Query
342	342	290	321	.311	269	235	275	273	273	274	273	270	275	20/6	2,75	2,75	<sup>2</sup> 2,75	Length	
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19
426	427	427	428	429	430.5	434	439.5	441	443	444	444.5	445	446.5	447	448	451	460.5	463	464	467	474.5	476.5	49	495	501.5	512
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263	266	263	810	810	271	490	269	343	245	ω ω	271	638	812	638	338	638	418	306	457	625	454	324	314	455	317	343
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## ALIGNMENTS

RP RX RA RT	D C C C C C C C C C C C C C C C C C C C	RESUL TRB2_ ID AC
SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3). MEDLINE-99121069; PubMed-9920877; Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.; "Characterization of genes encoding known and novel human mast cell tryptases on chromosome 16p13.3.";	Ol-FEB-1991 (Rel. 17, Created) Ol-FEB-1991 (Rel. 17, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Tryptase beta-2 precursor (EC 3.4.21.59) (Tryptase 2) (Tryptase II). TPSB2 OR TPS2. Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9006; [1] SEQUENCE FROM N.A. (VARIANT BETA-2). TISSUE=Lung; MEDLINE=90369005; PubMed=2203827; MILIET J.S., Moxley G., Schwartz L.B.; "Cloning and characterization of a second complementary DNA for human tryptase."; J. Clin. Invest. 86:864-870(1990). SEQUENCE FROM N.A. (VARIANT BETA-2). MEDLINE-93166209; PubMed=8434231; Blom T., Hellman L.; "Characterization of a tryptase mRNA expressed in the human basophil cell line KU912."; Scand. J. Immunol. 37:203-208(1993). [3] SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3). MEDLINE-90251647; PubMed-2187193; Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S., Caughey G.H.; "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine protease family."; Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).	T 1 HUMAN TRB2_HUMAN P20231; Q9UQ

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EMBL; M37488; AAA51843.1; -.
EMBL; M33492; AAA36780.1; -.
EMBL; M33493; AAA36780.1; -.
EMBL; S55551; AAD13876.1; -.
EMBL; AF099144; AAD17859.7; -.
EMBL; AF099146; AAD17858.1; -.
CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9443168; PubMed=10500112;

Sommerhoff C.P., Bode W., Pereira P.J.B., Stubbs M.T., Stuerzebecher J., Piechottka G.P., Matschiner G., Berg "The structure of the human betail-tryptase tetramer:
                                                                                                                               Pfam; PF00089; trypsin; T.

PRINTS; PR00722; CHYMOTRYPSIN.
SMARTS; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                            MEROPS; S01.027; -.
MEROPS; S01.242; -.
Genew; HGNC:14120; TPSB2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pereira P.J.B., Bergner A., Macedo-Ribeiro S
Matschiner G., Fritz H., Sommerhoff C.P., Bot
"Human beta-tryptase is a ring-like tetramer
a central pore.":
                                                                              PROPEP
                                                                                           SIGNAL
                                                                                                      Polymorphism;
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PDB; 1AOL; 23-MAR-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392:306-311(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x-ray Crystallography (3.0 angstroms).
medline=98180625; pubmed=9521329;
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                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POUNTION: TRYPTASE IS THE MAJOR NEUTRAL PROTESSE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.

SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differ by 3 residues.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYMORPHISM: There are two
                                                                                                                                                                                                                                                                                                      A37193; A37193.
B35863; B35863.
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                                                                                                                  Serine protease;
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31
74
121
121
224
155
                                                                                                        3D-structure.
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                         POTENTIAL.

ACTIVATION PEPTIDE.

TRYPTASE BETA-2.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ayesteh L., Blount
EMBL/GenBank/DDBJ
                                                                                                                    Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alleles; beta-II and
                                                                                                                    Glycoprotein;
                           Y SYSTEM.
Y SYSTEM.
Y SYSTEM.
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J databases.
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W.;
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                                                                                                                    Zymogen;
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Best Local Similarity:
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DISULFID
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                ACCGCCGCGCGCGTGCGTGCGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu
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                                                       ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
                                                                                                                                                                                                                                                             GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCCTCAGAGACCCTTCCCC
                                                                                                                                                                                                                                                                                           CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGTGGAGCCG
                        ValProLysLysPro
                                        GTCCCCAAAAAGCCG
                                                                                       AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCCAGGGCCTGTGCCCAG
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275 /
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99.59%
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HGP -> RDR
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K -> N (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> N (IN REF. 3).
2B27396C51F5C7A0 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TRB1\_HUMAN

STANDARD;

PRT;

275

AA

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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPc; 1.
PR051TE; PS50240; TRYPSIN_DOM; 1.
PR051TE; PS00134; TRYPSIN_HIS; 1.
PR05ITE; PS00135; TRYPSIN_ESR; 1.
Hydrolase; Serine protease; Signal;
                                                                                                                                                                                                                                                                                        entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q15661; Q15663; Q9H2Y4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, East annotation update)
16-OCT-2001 (Rel. 40, East annotation update)
                                                                                                                                                                                                                                                                                                                                  between
the Euro
use by
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                                                                                                                                                                                                                                                 EMBL;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases PR-1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PR-1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PR-1- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99121069; P
Pallaoro M., Fejzo
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MEDLINE=90251647; PubMed=2187193;
Wanderslice P., Ballinger S.M., Tam
               Alternative
SIGNAL
                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                     modified
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Hettiaratchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human mast cell tryptase: multiple cDNAs and genes serine protease family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of genes encoding known tryptases on chromosome 16p13.3.";
J. Biol. Chem. 274:3355-3362(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MASCELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                 ; P20231; 1A0L.
PS; S01.242; -.
W; HGNC:12019; TPSB1.
191081; -.
                                                                                                                                                                                                                   M33494; AAC83172.1; -. M33491; AAA36778.1; -. AF099144; AAD17860.1; -. AF206667; AAG35697.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 54-275
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                            splicing
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ants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FROM N.A. (ISOFORM 2).
H.P., Thomas P.S., Murphy B.N.,
King G., Heywood G.J., Huang C.,
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                                         Signal;
 POTENTIAL.
ACTIVATION
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                                        Glycoprotein;
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 PEPTIDE
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                        CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
                                                                                                                                                                                                            CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGATGAGCGCCTCCCA
                                                                                                                                                                                                                                                                         CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
                 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr
                                  CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT
                                                                                                                                                               ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
                                                                                                                                                                                                   {\tt ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuProcess} \\
                                                                                                                                                                                                                                       ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
                                                                                                                                                                                                                                                          GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCCCC
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P15157; Q9UQII; Q9H2Y5;
O1-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-tryptase precursor (EC 3.4.21.59) (Tryptase
         entities
or send a
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"Characterization of genes encoding known
tryptases on chromosome 16p13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=99121069; PubMed=9920877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of complementary
                                      modified
                                                                                                                                              -
                                                                                                                                                                                                                                                                 immunocytochemical localization, an
fluorogenic substrates.";
J. Biol. Chem. 262:1363-1373(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND
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                                                                                                                                                                                                                                                                                                           'Human pituitary tryptase: molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
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                                                                                                                                                                                    RESPONSE OF THIS CELL TYPE.
CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-,
with more restricted specificity than trypsin.
SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                              splicing
                                                               veen the Swiss Institute of Bioinfi
European Bioinformatics Institute.
                                                                                                                 produced by alternative splicing. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY
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E.;
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                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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           non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem. 274:3355-3362(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                   ing variants.";
  (NOV-1999) to the EMBL/GenBank/DDBJ databases
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Seidah N.G., Marci
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King G.,
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J., Huang C.,
                                                                                                                                                                                                                                                                                             forms, NH2-terminal sequence,
specificity with prohormone a
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SMART, SM00020; Tryp_SPC: 1.
PROSITE; PS00134; TRYPSIN_DOM;
PROSITE; PS00135; TRYPSIN_SER;
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PRINTS; PR00722; CHYMOTRYPSIN.
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InterPro; IPR001254;
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MEROPS; S01.015; -.
MEROPS; S01.143; -.
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                                  CCACAGTTCTACACCGCCCAGATCGGAGCGGAGCATCGCCCTGCTGGAGCTGGAGGAGCCG
                                                                     ACCGCCGCGGCGTGCGTGCGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
                                                                                                                                                         CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
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         GTGAAGGTCTCCAGCGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCCCC
                                                                                                                                                {\tt ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu}
ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro
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275 i
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;28; AAD17846.1; -.
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N-LINKED (GLCNAC. . .) (I

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R -> P (IN ALPHA-II).

/FTId=VAR_012102.

K -> Q (IN ALPHA-II).
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TR -> SQ (IN REF. 1)
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Matches:
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Mismatches:
Indels:
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  Reynolds D.S., Ste
Serafin W.E.;
"Different mouse n
of at least six di
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J. Biol. Chem. 266:3847-3853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P21845; Q61962;
01-MAY-1991 (Rel. 18, Created)
01-BUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
MCTC cell protease 6 precursor (EC 3.4.21.5
                                                                                                                                                                                                                                                                                                  "Expression of a mast cell tryptase U-937 and Mono Mac 6."; Scand. J. Immunol. 38:359-367(1993).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Leaden X A1; MEDLINE=94023807; P
                                                                                   SEQUENCE OF 32-54.
MEDLINE=90222202; PubMed=2326280;
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Mammalia; Eutheria;
                                                                                                                                                                                          SEQUENCE FROM N.A. (SHORT ISOFORM STRAIN=Leaden X A1;
MEDLINE=95048582; PubMed=7959952;
Huang R., Hellman L.T.;
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Nilsson K., Hellman L.;
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A38654; A38654.
PIR; D35646; D35646.
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ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and short form; are produced by alternative splicing. The short for is probably a non functional variant.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY
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RESPONSE OF THIS CELL TYPE.
CATALYTIC ACTIVITY: Preferential cleavage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., M57626; AAA39988.1; ... M57625; AAA39987.1; ... L31853; AAA39725.1; ... X78542; CAA55288.1; ...
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                                                                                     TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCCTC
                    ATCCACCCCAGTGGGTGCTGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTG
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                                                            TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu
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There are no restrictions ng as its content is in
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16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                             Canis familiaris (Dog).
                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last annotation Tryptase precursor (EC 3.4.21.59).
  between
            This
                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89352460; PubMed=2504277;
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
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SIMILARITY: BELONGS T
SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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InterPro; IPR001254; Sei
Pfam; PF00089; trypsin;
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00125; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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PROSITE; PS00135; TRYPSIN_SER; 1.
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SEQUENCE FROM N.A.
STRAIN-MGS/SEA; TISSUE=Intestine;
MEDLINE=95366971; PubMed=7639711;
Murakumo Y., Ide H., Itoh H., Tomita M., Kobayashi T.,
Maruyama H., Horii Y., Nawa Y.;
Maruyama of the cDNA encoding mast cell tryptase of Mongolian
Meriones unguiculatus, and its preferential expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See ) or send an email to license@isb-sib.ch)
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Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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Biochem. J. 309:921-926(1995).
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SEQUENCE
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                          GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC
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                                                                                                                 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGATGACCGCCTCCCA
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                                                                                                                                AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG
                                                                                                                                                                          {\tt SerGlyThrLeuCysTrpValThrGlyTrpGlyAsnIleAspAsnAspValSerLeuProperties} \\
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ValProLys
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183
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RESULT 7 MCT7\_MOUSE

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HSSP; FAUALIA, THE MEROPS; S01.026; -...
MGD; MGI:96943; Mcpt7.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001259; trypsin; 1.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
R SMART; SM00020; Tryp_SPC; 1.
R SMART; SM00020; Tryp_SPC; 1.
R PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q02844;
01-JUL-1993
01-JUL-1993
15-JUN-2002
            Hydrolase; Se:
Glycoprotein.
SIGNAL
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Ghildyal
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or send an email t
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EMBL; L00653; AAA39992.1; -.
EMBL; U42405; AAA97874.1; -.
EMBL; U42406; AAA97875.1; -.
EMBL; U42466; AAA97875.1; -.
                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation, characterization, and mouse mast cell protease 7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C57BL/6 mouse.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96162035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Austen K.F., Stevens R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93087489; PubMed=1454796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DBA/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Natural disruption of the mouse mast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 271:2851-2855(1996).
FUNCTION: TRYPTASE IS THE MAADOR NEUTRAL PROTEASE PRES
CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DE
RESPONSE OF THIS CELL TYPE.
CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Ly
with more restricted specificity than trypsin.
ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown
                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN MATURE SEROS MUCOSAL MAST CELLS AND IS EXPRESSED ONLY TRANSIENTLY STAGE OF IN VITRO MAST CELL DIFFERENTIATION.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                              truncated form; are produced by alternative splicing. The alternative splicing event is due to a G to A point mutation the exon 2/intron 2 splice site and causes loss of protein expression. The alternatively spliced transcript is only four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation.
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3 (Rel. 26, 26, 20)

2 (Rel. 41, 20)

protease 7 p
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Sci. U.S.A. 89:11174-11178(1992).
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Rodentia;
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----aor (EC 3.4.21.59)
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                                                                                       GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGAGGCGTGGTC
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                                                                                                                                                                                                                                                                                        GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATA
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                 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC
                                                                                                                                               HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly
                                                                                                                                                                                   CGCATCGTCCGTGACGACATGCTGTGTGCCGGGGAACACCCGGAGGGACTCATGCCAGGGC
                                                                                                                                                                                                                     {\tt IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnValue}
SerTrpGlyGluGlyCysAlaG
                                                                      {\tt AspSerGlyGlyProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValValVal}
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                                                                                                                           InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCT6_RAT STANDARD; PRT; p50343; p97593; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence to 16-OCT-2001 (Rel. 40, Last annotation Mast cell protease 6 precursor (EC 3 MCPT6 OR MCP6
   CHAIN
ACT_SITE
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CARBOHYD
                                                                                                   Signal.
SIGNAL
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J. E>
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Peritoneal mast MEDLINE-97149430; PubMed-8996238; Lutzelschwab C., Pejler G., Aveskogh M., Hellm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Peritoneal mast cells
MEDLINE=96015171; PubMed=853
Ide H., Itoh H., Tomita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
                                                                                                                       Hydrolase;
                                                                                                                                                                                                                      EMBL; D38455; BAA07486.1;
EMBL; U67909; AAB48262.1;
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                      "Secretory granule proteases in rat mast cells. Cloning of different serine proteases and a carboxypeptidase A from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maruyama H., Osada Y., Nawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cDNA sequencing and expression of J. Biochem. 118:210-215(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                            tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       RESPONSE OF THIS CELL TYPE.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Ly with more restricted specificity than trypsin.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE
                                                                                                                                                                                                                                                                                                                                                                               cell populations.";
Exp. Med. 185:13-29(1997).
FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL CELLS, AND IS SECRETED UPON THE COUPLED
                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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non-profit institutions as long
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PubMed=8537314;
                                                                                                                       protease;
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274
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73
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223
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210
247
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Last annotation update)
precursor (EC 3.4.21.59)
                                                                                                                      Glycoprotein;
  BY SIMILA
BY SIMILA
BY SIMILA
N-LINKED
                                                CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                              ACTIVATION PEPTIDE.
MAST CELL PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I
Sciurognathi; Muridae;
           Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat mast cell tryptase.";
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  (GLCNAC.
                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hellman L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi
                                                                                                                     Multigene
                                                                                                                                                                                                                                                                                                                                                                               PROTEASE PRESENT IN MAST ACTIVATION-DEGRANULATION
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  (POTENTIAL)
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Query Match:
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MCT7_RAT STAN
P27435; P27436;
01-AUG-1992 (Rel. 2
01-NOV-1997 (Rel. 2
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CONFLICT
CONFLICT
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                                                                    LeuAspTrpIleHisArgTyrValProGlnArg
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I -> T (IN REF. 2).
I -> T (IN REF. 2).
                              PRT;
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Matches:
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CCCCTCGAGAAAAGA-----ATCGTCGGGGGTCAGGAGCCCCCAGGAGCAAGTGGCCC
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{\tt GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspValPro}
                                                                                                                                                                                                                                                                                                                                                                                   GACAATGATGAGCGCCTCCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTGGAGCTGGAGGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAsnArgThrValValHisProHisTyrTyrThrValGluAspGlyAlaAspIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrAlaAspGlnLeuLeuThr
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                                                                                                                                                                       IleValGlnAspGlyMetLeuCysAlaGlyAsnThrArgSerAspSerCysGlnGlyAsp
                                                                                                                                                                                                                                                                                                                                            AspSerAspGluProLeuLeuProProTyrProLeuLysGlnValLysValProIleVal
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Pfam; Proceed: CHrmca...

PRINTS; PR00722; CHrmca...

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.
                                                                                                                                                                       PIR; A23698; A23698.
PIR; S21275; S21275.
HSSP; P20231; IAAO.
MEROPS; S01.026; -.
MEROPS; S01.143; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Secretory granule proteases in rat mast cells. Cloning of 10 different serine proteases and a carboxypeptidase A from various cell populations.";

J. Exn Med Tor
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                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as form modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                     EMBL; U67910; AAB48263.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       leupeptin-sensitive serine endopeptidase induced rat mammary tumour "; Biochem. J. 283:209-216(1992).
-!- FUNCTION: TRYPTASE IS THE MAJOR NEUTI CELLS, AND IS SECRETED UPON THE COUPI RESPONSE OF THIS CELL TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braganza V.J., Simmons W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Skin; MEDLINE=91242400; PubMed=2036367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley;
MEDLINE-97149430; PubMed-8996238;
Lutzelschwab C., Pejler G., Avesk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin).
MCPT7 OR MCP7
  ACT_SITE
                                      SIGNAL
                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 29-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 29-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92231826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Tryptase from rat skin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel.
                                                  Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Separation, purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp.
                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Preferential with more restricted specificity SUBUNIT: HOMOTETRAMER. SUBCELLULAR LOCATION: RELEASED FI
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                MAST CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell
                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grubbs C.J
                                                                                                                                                                                                                                                                                                                                                                        GLYCOSYLATED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease
                                                  family.
                                                                                                                                                                                                                                                                                                                                                                                  SPECIFICITY: MAST CELLS
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e 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase.
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POTENTIAL.
ACTIVATION PEPTIDE.
MAST CELL PROTEASE 7
CHARGE RELAY SYSTEM
                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; i
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                            FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUPLED
  RELAY SYSTEM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                   cleavage:
than tryp:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properties.";
                                                              Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                   trypsin
                                                                                                                                                                                                                                                                        http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                            S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE PRESENT IN MAST ACTIVATION-DEGRANULATION
                                                                                                                                                                                                                                                                                                                                                                                                            SECRETORY
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  SIMILARITY).
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CONFLICT
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pIleTyrArgTyrValProLys
                   GATCCACCACTATGTCCCCAAA
                                               gLeuCysAspLeuLysTyrHisLysGlyLeuAsnThrGlyAspAsnValHisIleValAr
                                                                                                                                                                          CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG
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                                      uGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTr
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71.26%
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
V-LINKED (GLCNAC...
W-V (IN REF. 3).
NDT -> WLP (IN REF. 3).
NDT -> WLP (1N REF. 3).
 27
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Matches:
Conservative:
Mismatches:
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Gaps:
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RESULT 10
TRYT_SHEEF
                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                        Percent Similarity:
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PFAm: PFOOUD.,
PRINTS; PRO0722; CHYMUL...
SMARP; SW00020; Tryp_SPc; 1.
R PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09XSM2;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
15-JUN-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S.,
Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.;
"CDNA sequence of two sheep mast cell tryptases and the differential
expression of tryptase and sheep mast cell proteinase-1 in lung,
dermis and gastrointestinal tract.";
Clin. Exp. Allergy 30:818-832(2000).
-i-FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
RESPONSE OF THIS CELL TYPE.
-i-CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
with more restricted specificity than trypsin.
-i-SUBCELLUAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
17-yptase 2 precursor (EC 3.4.21.59).
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Rum
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                    PROPEP
CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.143; -
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                                                                                                                     No : :
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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                       3.33e-53
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84.08%
73.06%
70.64%
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Matches:
                                            Conservative:
Mismatches:
                            Indels:
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minantia; Pecora;
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(BY)
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RESULT
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                                                                                          Tryptase MCT7.
                                                                                                                                           TRYT_PIG
Q9N2D1;
                    SEQUENCE FROM N.A. TISSUE=Lung;
                                                             Eukaryota;
Mammalia; I
                                                                                                             16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
           MEDLINE=20285343;
                                                                                Sus scrofa (Pig)
                                                  NCBI_TaxID=9823;
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                                                                                                                                                                                              ValProGlnGluPro
                                                                                                                                                                                                                 GTCCCCAAAAAGCCG
                                                                                                                                                                                                                                                                                                                     CysAlaGlyAspGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
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                                                                                                    precursor
  Shiota M.,
                                                            ; Metazoa;
Eutheria;
                                                                                                                                                      STANDARD;
                                                                                        . 40, Createw,
. 40, Last sequence upd:
L. 41, Last annotation u
sor (EC 3.4.21.59).
          PubMed=10824103;
 Ohuchi M.,
                                                           Cetartiodactyla;
                                                                     Chordata;
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                                                           Craniata; Vertebrata;
actyla; Suina; Suidae;
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                                                             Euteleostomi;
Sus.
  Murakami
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50244; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mast cell tryptase from pig lungs triggers infection by pure mast cell tryptase from pig lungs triggers infection by pure mast cell tryptase from pig lungs triggers infection."; Sendal and influenza A viruses. Purification and characterization."; Eur. J. Biochem. 267:3189-3197(2000).

-i. FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

-i. CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.

-i. SUBCURIT: HOMOTETRAMER (By similarity).

-i. SUBCULLUAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
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the Euro
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SIGNAL
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GlyGluGlnHisLeuTyrTyrGlnAspArgLeuLeuLeuValSerArgIleIleValHis
                                                                               ThralaalaHisCysPheGlyProGluLysAlaAspProLeuTyrIleArgValGlnLeu
                                                                                                                                                                                                        CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
                                                                                                                                                                                                                                                                              IleValGlyGlyLysGluAlaProGlyHisLysTrpProTrpGlnValSerLeuArgCys
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Pallaoro M., Fejzo M.S., Shayesteh L.,
"Characterization of genes encoding knot cryptases on chromosome 16p13.3";
J. Biol. Chem. 274:3355-3362(1999).
                                                                                                                                                                                                                                                                                                                                TRYD_HUMAN STANDARD; PRT; 235 AA O9BZJ3; Q9HZY6; O95824; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update Putative tryptase delta precursor (EC 3.4.2 like) (HmMCP-3-11ke tryptase III).
           "Molecular cloning and characterization of novel
and splicing variants.";
                                                          Wang
                                                                                                         "Human mouse mast cell pseudogenes.";
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                   Hunt J.E.
                                               Hettiaratchi A., King
                                                                       SEQUENCE
                                                                                             J. Allergy Clin. Immunol. 107:315-321(2001).
                                                                                                                                  Min H.K., Kambe N.,
                                                                                                                                                MEDLINE=21101554;
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H.P., Thomas P.S., Murphy B.N.,
King G., Heywood G.J., Huang C.,
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1
PRINTS; PR00722; CHYMOTRYPSIN.
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PROSITE; PS50240; TRYPSIN_DOM; 1.
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EMBL; AF318074; AAK12909.1; -.
EMBL; AF206664; AAG35694.1; -.
HSSP; P20231; 1AAO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: This seems to be the product of a
GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCCTTCCCC
                                                                                                CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGCTGGAGCCG
                                                                                                                                               ThrAlaAlaHisCysValGluProAspIleLysAspLeuAlaAlaLeuArgValGlnLeu
                                                                                                                                                             ACCGCCGCGGCGTGCGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
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                                                  ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro
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ACTIVATIVE TRYPTASE DELTA.
CHARGE RELAY SYSTEM (BY SI)
BY SIMILARITY.
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InterPro; IPR001254; Ser_protease_Try.
Pfam; Pf00089; trypsin; 1.
PRINTS; PR00722; CryMoTryPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89352460; PubMed=2504277; Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.; Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.; "Molecular cloning of data cell tryptase and a related protease: structural evidence of a unique mode of serine protease activation."; Biochemistry 28.4148-4155(1989).
-i- FUNCTION: MAST CELL PROTEASE.
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NCBI_TaxID=9615;
[1]
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PIR; B32410; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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01-NOV-1990 (Rel.
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PROSITE; PS00134;
PROSITE; PS00135;
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CARBOHYD
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STRAIN-129/Sv, and BALB/C;

MEDLINE-99/452974; PubMed-10521469;

Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y.,

Friend D.S., Krilis S.A., Stevens R.L.;

"Identification of a new member of the tryptase family human mast cell proteases which possesses a novel COOH hydrophobic extension.";

J. Biol. Chem. 274.30784-30793(1999).
                                                                                                                                                                                                                                                                                                      CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF175760; AAF03698.1;
EMBL; AF175523; AAF03696.1;
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00134; PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1349391; Tpsg1.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001534; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tryptase gamma precursor TPSG1 OR TMT.
                                                                                                                                                                                                                                                                                                                                          Transmembrane
                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: Expressed in many tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                              -598-982-20
                                                                                                                              No. .
  29
                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
{\tt ArgIleValGlyGlyHisAlaAlaProAlaGlyThrTrpProTrpGlnAlaSerLeuArg}
                       AGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S01.028; -
                                                                                                                                                                                                                                                                                                                                                    Serine
                                                                                                                                                                                                  70
117
214
18
55
151
184
210
                                              (1-771) x TRYG_MOUSE
                                                                                                                                                                                                                                                                                                                                                               TRYPSIN_HIS; 1.
TRYPSIN_SER; FALSE_NEG.
                                                                             1.13e-28
608.50
60.63%
48.43%
41.74%
                                                                                                                                                                                                                                                                                                                                                    protease;
                                                                                                                                                                                                                                                                                                                                                                                     TRYPSIN_DOM;
                                                                                                                                                                                       16
28
311
297
70
117
214
137
71
220
230
238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC
                                                                                                                                                                 W.
                                                                                                                                                                                              POTENTIAL.

CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM).

INTERCHAIN (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                    Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4.21.-) (Transmembrane
                                                                                                                                                                N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
7FC9D6EF6A2A8808 (
                                                                                                                                                                                                                                                                                                      TRYPTASE GAMMA LIGHT TRYPTASE GAMMA HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                              (1-311)
                                                                             Mismatches:
Indels:
                                                                                                       Length:
Matches:
Conservative:
                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel COOH-terminal
                                                                                                                                                                 CRC64;
                                                                   311
123
31
81
19
                                                                                                                                                                             .) (POTENTIAL)
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(BY
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                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                         SIMILARITY)
SIMILARITY)
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                                                                                                                                                                                                                                                                                 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang
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TRYGARD OCCOORS
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[2]
SEQUENCE FROM N.A.
MEDLINE-99452974; Put
Tang Y., I
                                                                                                                                                                            Q9NRR2; Q9NRQ8; Q9C015; Q9UBB2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane
TPSG1 OR TMT.
                                                                             Caughey G.H., Raymond W.W., Blount J.L., Wolters P.J., Verghese G.M.;
                                                                                                   SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND MEDLINE=20302813; PubMed=10843716;
                                                                                                                                        Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                TRYG_HUMAN
                                            "Characterization of human gamma-tryptases, chromosome 16p mast cell tryptase and prost. J. Immunol. 164:6566-6575(2000).
                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                 ValGlnLeuSerSerProValAlaLeuSerSerGlnValGlnProValCysLeuProGlu 140
                                                                                                                                                                                                                                                                                                                                                        GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                 {\tt GluGlyGluProLeuLysProProTyrAsnLeuGlnGluAlaLysValSerValValAsp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaSerAlaAspPheTyrProGlyMetGlnCysTrpValThrGlyTrpGlyTyrThrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCGGGAGCAGCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG
                                                                                                                                                                                                                                                                                        AsnTrpIleHisHisHisIleProGluAlaGlyGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                       IleGlnProAspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValLysThrCysSerGln-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrAlaAlaHisCysPheSerGlySerValAsnSer---SerAspTyrGlnValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
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                                                                                                                                                                                                                                            STANDARD;
  PubMed=10521469; ., Feyfant E., Sa
                                                                                                                                                                                                                                             PRT;
   Sali A.,
                                                                                                                                                                                                                                             321
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ene families.";
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                      Score:
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Best Local Similarity:
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Alignment
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PROSITE; PS0013; TRYPSIN_DOM; 1

PROSITE; PS0013; TRYPSIN_HIS; 1

PROSITE; PS0013; TRYPSIN_HIS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF191031; AAF76457.1; -
EMBL; AF195508; AAF76458.1; -
EMBL; AF175759; AAF03697.1; -
EMBL; AF175522; AAF03695.1; -
EMBL; AF223563; AAG48852.2; -
HSSP; P00763; IDPO.
                                                                                                                                                    CONFLICT
SEQUENCE
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ACT_SITE
ACT_SITE
ACT_SITE
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"Organization and alternative splicing of CACNAlH.";

"Organization and alternative splicing of CACNAlH.";

"Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).

-!- TISSUE SPECIFICITY: Expressed in many tissues.

-!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrophobic extension.";
J. Biol. Chem. 274:3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:14134; TPSG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the property of the p
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                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                              VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
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                                                                              NO.:
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                                                                                                     Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S01.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 220-321 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease;
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321 /
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TRYPSIN_SER; FALSE_NEG
8.39e-28
593.50
61.89%
48.77%
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BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (1
M -> V (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal;
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                                                                                                                                                                           /FTId=VAR_012101
W -> S (IN REF. ]
                                                                                                                                                                                                                                                                                                                               /FTId=VAR_012098.
S -> T (IN GAMMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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/FTId=VAR_012099.
L -> I (IN GAMMA-II).
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I -> M (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                          /FTId=VAR_012100.
L -> F (IN GAMMA-II).
                                                                                                                                                    -> S (IN REF. 1)
FFF7B06E3C4A962D
                                                 Length:
Matches:
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Conservative: Mismatches:

Query DB: US-09-	Match: 40.71% Indels: 13 Gaps: 6 598-982-20 (1-771) x TRYG_HUMAN (1-321) 16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA
Qу Db	76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGT :::
Фу	136 CTGACCGCCGGGGGGTGGGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGC.
Qу	196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCCGGTCGCCGGTCAGCAGGATCATCGTG
Qу Db	256 CACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTG
Оу	310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCCTGCCCTCAGA
Оy	370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATG.
Дy	430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC
Qy Db	490 TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
Qy Db	550 GACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCC
QУ	610 CTGGTGTGCAAGGTGAATGGCACCTGGCTGGCGGGGGGGG
Qу	670 TGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCC         :::
Qу	730 CACCACTATGTC 741 266 ArgargHisile 269
arch	completed: January 31, 2003, 06:54:08

Search completed: January 31, 2003, 06:54:08 Job time : 34.5 secs



2 1387 95.1 249 4 US-09-079-970A-5 2 1368 93.8 245 4 US-09-079-970A-6 Sequence 5, Appli 3 1368 93.8 274 2 US-09-016-366A-21 Sequence 21, Appli 4 1368 93.8 274 2 US-09-016-366A-21 Sequence 16, Appl 5 1363 93.5 273 2 US-09-016-366A-19 Sequence 16, Appl 6 1363 93.5 273 2 US-09-016-366A-19 Sequence 14, Appl 7 1344 92.2 267 2 US-09-016-366A-23 Sequence 23, Appl 8 1344 92.2 267 2 US-09-016-366A-23 Sequence 14, Appl 9 1274 87.4 275 2 US-09-016-366A-17 Sequence 17, Appl 10 1274 87.4 275 2 US-09-016-366A-15 Sequence 17, Appl 11 1274 87.4 275 2 US-09-016-366A-15 Sequence 12, Appl 12 1092 74.9 276 2 US-09-016-366A-15 Sequence 15, Appl	Result Query No. Score Match Length DB ID Description	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Database: Issued_Patents_AA:*  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*  3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*	Command line parameters:  -MODEL-frame+_n2p.model -DEV=xlh -Q-/cgn2_1/USCPTQ_spool/USC9598982/runat_27012003_073718_19604/app_query.fasta_1.967 -DB-Issued_Patents_AA -QEMT=fastan -SUFFIX-n2p.rai -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -USER=USC9599892_GCGN_11_4_@runat_27012003_073718_119604 -NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 525148	Searched: 262574 seqs, 29422922 residues	Scoring table: BLOSUM62  Xgapop 10.0 , Xgapext 0.5  Ygapop 10.0 , Ygapext 0.5  Fgapop 6.0 , Fgapext 7.0  Delop 6.0 , Delext 7.0	Title: US-09-598-982-20 Perfect score: 1458 Sequence: 1 999cccctcgagaaaagaatcgtgaagcggccgccgtcgt 771	Run on: January 31, 2003, 06:53:20 ; Search time 16.5 Seconds (without alignments) 2749.706 Million cell updates/sec	OM nucleic - protein search, using frame_plus_n2p model	GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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1, Appl	1, Appl	59, App	3, Appl		19, App	62, App	64, App	83, App	82, App	25, App	2, Appl	53	8, Appl	3, Appl	7, Appl	66, App	11, App	12	9, Appl	7, Appl	10	6, Appl	6, Appl	6, Appl	4, Appl	4, Appl	4, Appl	e 6, Appl	e 5, Appl	equence 3, Appl	е 8	1, App

## ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Niles, Andrew L.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
ITILE OF INVENTION: Enzymatically-Active Recombinant Human
ITILE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 37,170
REGISTRATION NUMBER: 37,170
REGISTRATION NUMBER: 31-2100
TELEPONE: (608) 831-2106
INFORMATION: 19R SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS: Sequence 5, Application US/09079970A Patent No. 6274366 GENERAL INFORMATION: RESULT 1 US-09-079-970A-5

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Percent Similarity:
Best Local Similarity:
Query Match:
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       Sequence 6, Application Patent No. 6274366
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (608) 831-210
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Enzymatically-Active Recombinant Human TITLE OF INVENTION: Beta-Tryptase and Method of Making Sam NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                     No . .
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CITY: Madison
STATE: WISCONS:
COUNTRY: U.S.A
ZIP: 53717-191
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TYPE: a
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                                    ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
                                                                                   ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro
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Matches:
Conservative:
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            Alignment Scores:
                                 US-09-016-366A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21,
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APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                               REFERENCE/DOCKET NUMBER: BC TELECOMMUNICATION INFORMATION: 617-720-3500
                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
  No . :
                                            LENGTH: 274 amino TYPE: amino acid STRANDEDNESS: sinc TOPOLOGY: linear
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STREET: 600 A
CITY: Boston
STATE: MA
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                                                                                                                    TELEFAX:
                                                                                                                                                                NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/016,366A
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Best Local Similarity:
Query Match:
                                                                                                                  US-08-978-404B-16
                                                                                  Sequence 16, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                      APPLICANT: Stevens, R
TITLE OF INVENTION: M
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                               CORRESPONDENCE ADDRESS:
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                                                              Richard L.
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US-09-598-982-20 (1-771) x US-09-016-366A-21 (1-274)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat

IBM Compatible Diskette STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECAMMUNICATION INFORMATION:
TELECHONE: 617-720-3500
TELECAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 274 amino acids
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                          439
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STRANDEDNESS: single
TOPOLOGY: linear
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SOFTWARE: FastSE(
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CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGGAGCCG 318
                                                                                                                                                                                                     CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
                                                ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 149
                                                                                                                 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCCTCAGAGACCTTCCCC 378
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Conservative:
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Alignment Pred. No.: Score: Score: Percent Si Best Local Query Matc DB:	INFO SE	TERLI			8	Ć	S A A H B Z	ESULT 5 IS-09-01 Sequen Patent	Qy 739 Db 270	Qy 679 Db 250	Оу 619 Db 230	Oy 559 Db 210	Qy 499 Db 190
Scores: milarity: Similari h:	ATION ENCE NGTH: PE: PE: POLOG	NAME: Plumer, Elizabeth R REGISTRATION NUMBER: 36,6: REFERENCE/DOCKET NUMBER: 1 TELECOMMUNICATION INFORMATION TELEPHONE: 617-720-3500 TELEPHONE: 617-720-2441 TELEX	LAING DATE: LASSIFICATION DR APPLICATION: PPLICATION: CLING DATE: DRNEY/AGENT	OPERATING SYSTEM: SOFTWARE: FastSE URRENT APPLICATION APPLICATION NUMBE	210 EAD	ADDRESSEE: WASTREET: Boston STRIE: MA STATE: MA	APPLICANT: Stevens, R APPLICANT: Stevens, R APPLICANT: Huang, Chi TITLE OF INVENTION: M TITLE OF INVENTION: I NUMBER OF SEQUENCES:	6-366A-19 ce 19, Appl No. 595543	GTCCCCAAAAAGCCG				
1.33e- 1363.0 99.18a ty: 99.18a 23.48a	TFOR SEQ ID NO: CHARACTERISTICS: 273 amino acids amino acid DNESS: single Y: linear	r, Elizabeth R. NUMBER: 36,637 CKET NUMBER: BO CKET NUMBER: BO CON INFORMATION: 617-720-3500 7-720-2441	January 3 ON: 530 ION DATA: NUMBER: 60 05-FEB-19 INFORMATIC	SYSTEM: DOS FastSEQ for ICATION DATA:	1 FOF iske		ic AS NH	us	AAGCCG 753        LysPro 274	CCTGGCATCTA           ProGlyIleTy	GCACCTGGCT           SlyThrTrpLe	AACACCCGGAG            snThrArgAr	CTTGGCGCCTA            CeuGlyAlaTy
102	19: 1s	th R. 36,637 R: B0801/70 MTION:	7,0	Windows Ve	)le	field & S venue	ard L. CELL P BITORS	/09016366A		ACACCCGTGTC              /rThrArgVal	GCAGGCGGGC	GGACTCATGO	CACGGGAGAC             ThrGlyAsp
Length: Matches: Conservative Mismatches: Indels: Gaps:		7093		ersion 2.0 56A		acks, P.C.	ROTEASE PEPTID			DACCTACTACT!             ThrTyrTyrL	GTGGTCAGCTO	)CAGGGCGACT(             GlnGlyAspS	GACGTCCGCA            AspValArgI
273 243 e: 0 0							Œ			CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCACTAT 	AAGGTGAATGGCACCTGCCTGCAGGCGGGCGGGCTCAGCTGGGGCGAGGCCTGTGCCCAG 	TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTG 	AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 
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US-09-598-982-20

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Sequence 14, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
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Query Match:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 25-Nov-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
TOPOLOGY: lin
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REFERENCE/DOCKET NUMBER: B00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/0:
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth I
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FastSEQ for Windows Version
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Matches:
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US-08-978-404B-14

APPLICANT: Stevens, TITLE OF INVENTION: TITLE OF INVENTION:

Richard L. MAST CELL FIBRINOGEN

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

E: Wolf, Greenfield 600 Atlantic Avenue

ADDRESSEE: Wolf,
STREET: BOS Atlar
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FO
MEDIUM TYPE: Dis)

READABLE FORM: TYPE: Diskett

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                                US-09-598-982-20 (1-771) x US-09-016-366A-23 (1-267)
                                                              Query Match:
                                                                         Best Local Similarity:
                                                                                  Percent Similarity:
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Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                 NAME: Plumer, Elizabeth R.
REGIZHION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/016, FILING DATE: January 30, 1998 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/037,090
                                                                                                                                                                                                                                                                                    FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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                                                                                                        No.:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
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                                                                                   COUNTRY:
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Sequence 18, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                       APPLICANT: Stevens, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
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APPLICATION NUMBER:
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                                   Version
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FILING DATE: 2 CLASSIFICATION:

25-NOV-97

APPLICATION NUMBER:

60/032,354

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 267 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: 617-720-3500
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                                                                                                                                                                                                                                                                                                                                                      ACCGCCGCGGGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
                                                                                                                                                                                                            CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
                                                                                                                                                               {\tt ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro}
                                                                                                                                                                           CCGGGGATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
                                                                                                                                                                                                                                                                                                           CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
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 AAGGTGAATGGCACCTGCCAGGCGGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCCAG
                                                                                AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG
                                                                                                                                                                                                                                                                                                                                 CGGGAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal}
                                                                     LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu
                                                                                                                  ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
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            Percent Similarity:
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Query Match:
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                                                                              Alignment Scores:
                                                                                                         US-08-944-483-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART D.
APPLICANT: STEWAR D.
TITLE OF INVENTION: NOVEL SERII
TITLE OF INVENTION: AND METHOD:
TITLE OF INVENTION: OF THE PRO:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                    TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 245 amino acid
                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ADDRESSEE: Abbott Laboratories
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: I
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                                                                                                                                                                                                                                                                            NAME: Becker, Cheryl REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CLASSIFICATION:
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                             TYPE:
                                                                                                                                                                                                                        TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLPITTS, TRACEY L.
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                                                                                                                                   linear
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                                                                                                                                                                     amino acids
                                                                                                                    No. 6232456e
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1274.00
94.69%
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87.38%
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AND METHODS USEFUL FOR DETECTING
OF THE PROSTATE
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, EDWARD N.
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US-09-598-982-20 (1-771) x US-08-944-483-69 (1-245)

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Sequence 17, Application US/09016366A Patent No. 5955431 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
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Best Local Similarity:
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FILING DATE: 05-FEB-1997
ATTORNEY_AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE OF OCCUPANT NUMBER: 00001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500 TELEFAX: 617-720-2441
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APPLICATION NUMBER: US
FILING DATE: January 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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SOFTWARE: FastSEQ for Windows Version
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Matches:
Conservative:
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Best Local Similarity:
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US-08-978-404B-12
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                                                                                             US-09-598-982-20 (1-771) x US-08-978-404B-12 (1-275)
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SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B08(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
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ADDRESSEE: Wolf, Greenfield &
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SOFTWARE: FastSE(
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US-09-016-366A-15
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APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INFIBITORS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                              COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                      ADDRESSEE: Wolf, Greenfield STREET: 600 Atlantic Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr
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PRIOR APPLICATION DATA:

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SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                   GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro
                                                                                                                                                         GACAATGATGAGGGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
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                                                                                                 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGGAGACGACGTCCGC
                                                                                                                                         AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal
                                                                                                                                                                                                GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCAGCTCTACTACCAGGACCAGCTGCTGCCG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGGGGTGGTCAGC
                                          ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGCCGAC 597
                                                                                                                                                                                                                           GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
                                                                                                                                                                                                                                                                                                                                                                     GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104
                             IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAsp 224
                                                                                                                                                                                                                                                                                                              LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124
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Matches:
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US-08-978-404B-21
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                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  TOPOLOGY: 1i
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ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth I
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro
                                                                                                                                                                      Similarity:
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MAST CELL PROTEASE THAT CLEAVES
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Sequence 8, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: Stevens, TITLE OF INVENTION: TITLE OF INVENTION:
                FILING DATE: 25-NOV-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                          COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                   ADDRESSEE: WO.
STREET: 600 A:
CITY: Boston
STATE: MA
                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows
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     DATE:
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     04-DEC-1996
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MAST CELL PROTEASE THAT CLEAVES
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: No. 5
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                                         CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
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                                                                                                 CysAlaGlyAsnGluGlyHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
                                                                                                              TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
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270 amino acids
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US-08-978-404B-8

RESULT 14

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                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stevens, I
TITLE OF INVENTION: N
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                             .
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500 TELEPAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C
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CITY: E
STATE:
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                                                                                                                                                                                                                                                                                                                                        LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM:
  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
GGGCCCCTCGAGAAAAGA-----ATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGG
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/ENTION: MAST CELL PROTEASE THAT CLEAVES
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Matches:
Conservative:
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Indels:
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                                                            AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC
                                                                                               HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly
                                                                                                                                                                                                             ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGCGGAGACGTC:::||||||||:::|||
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TyrLeuAspTrpIleHisHisTyrValProLys
                         TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
                                                                                                                                                             CGCATCGTCCGTGACGACATGCTGTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGC
                                                                                                                                                                                                IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnVal
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Search completed: January 31, 2003, 07:00:10 Job time : 22.5 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - protein search, using frame\_plus\_n2p model

January 31, 2003, 05:24:20 ; Search time 46 Seconds

(without alignments)
4466.793 Million cell updates/sec

Perfect score: Title: US-09-598-982-20 1458 Run on:

gggcccctcgagaaaagaat.....cgtgaagcggccgccgtcgt 771

Scoring table: Xgapop 10.0 , Ygapop 10.0 , Ygapop 6.0 , I Fgapop 6.0 , I Delop 6.0 , I BLOSUM62 Xgapext Ygapext Fgapext Delext

Searched: 908470 seqs, 133250620 residues 0.5 7.0 7.0

Total number of hits satisfying chosen parameters:

1816940

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match

Listing first 45 summaries 100%

Command line parameters:
-MODEL=frame+\_n2p.model -DEV=xlh

-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A\_Geneseq\_101002:\* 1: /SIDS2/gcgdata, 18: 19: 20: 21: 22: 23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT: \*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query	о¥С	_
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	Score	Match	Length	DB	ID	Description
1	1393	95.5	249	23	AAU12009	man beta-II tr
Ν	1388	95.2	249	23	AAU12017	beta-II
ω	1387	5	249	21	AAY55011	beta-try
4	1387	95.1	249	23	AAU12007	binant
ഗ	1384	4.	249	23	AAU12011	Н
6	1384	94.9	249	23	AAU12012	beta-II
7	1382	4.	249	23	AAU12006	beta-I t
œ	1379	4.	249	23	<b>N</b> 3	n beta-II
9	1379	94.6	249	23	AAU12019	beta-II
10	1379		249	23	AAU12020	n beta-II
11	1374	4.	245	23	01	n beta-II
	1374	4	249	23	AAU12018	Η
13	1369	ω.	245	23	AAU12021	Human beta-II tryp
14	1368	Ψ	245	23	AAU12008	Recombinant human
15	1368	ω ·	274	19	AAW64240	Human mast cell tr
16	1368	ω.	274	19	AAW63175	Human mast cell tr
17	1365	ω.	245	23	AAU12015	Human beta-II tryp
8	1365	93.6	245	23	AAU12016	Human beta-II tryp
¥ 5	1363	٠.	245	) \ 	AAY55ULU	beta-trypta
2 6	1363	υ u	273	10	AAW64738	Human mast cell tr
22	1363	ω.	273	19	AAW63174	n mast cell
23	1361	ω.	244	20	S	lung mast
24	1360	ω.	245	23	K1	beta-II tr
25	1360	ω.	245	23	0	4
26	1360	93.3	245	23	02	
27	1355		245	23	02	
28	1344	.2	267	19	4	mast cel
29	1344	2	267	19	AAW63176	e11
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	1274	87.4	275	19	AAW64237	cell
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41	1039	<u>'</u>	273	19	AAW64235	
42	1006	69.0	275	21	AAY81826	
43	702	48.1	190	20	AAW68539	no aci
44		47.9	190	20	854	Amino acid sequenc
45	684.5	46.9	269	19	AAW64236	Canine homologue o

## ALIGNMENTS

RESULT 1 AAU12009 AAU12009 standard; Protein; 249

09-APR-2002 (first entry)

Human beta-II tryptase active site mutant H44A #1.

enzyme; mutant; mutein. Human; proteolytic tryptase; protease; recombinant beta-II tryptase;

PD XXX Homo sapiens.

Synthetic

WO200198470-A2

27-DEC-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a
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           ATCCACCACTATGTCCCCAAAAAGCCG 753
                                              AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly
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beta-tryptase. The DNA construct is useful for transforming host cells to CC express, post translationally process and secrete enzymatically active chuman tryptase. The method is useful for the production of large amounts of tryptase with defined specifications. The transformant is useful for conformant is useful for conformant is useful for conformatically active crystallographic studies, combinatorial library screens and x ray conformant of tryptase agonists and/or antagonists, is useful for checked allows for the compounds which act as tryptase inhibitors, can be used in screening for compounds which act as tryptase inhibitors, can be used in screening for compounds which act as tryptase inhibitors, can to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in compounds which compounds to post-expression or post-purification modifications or manipulations to initiate tryptase activity and it has enzymatic activity which compares favourably with cadaveric tryptase. The availability of enzymatically cative tryptase facilitates the large scale screening of combinatorial conformations the understanding of the biological significance of tryptase in levels of tryptase in tryptase can be used to detect low construct of tryptase. The tryptase can be used to detect low
                                                   Percent Similarity:
                                                                                                   Alignment
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y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the human beta-tryptase. The invention relates to DNA expression construct comprising (5' to 3') a promoter linked signal sequence which is linked to a sequence encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 43-44; 50pp; English.
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DB; AAZ40175.
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                                                                                                           Homo sapiens.
Synthetic.
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                                                                                                                                                                        proteolytic tryptase; protease; recombinant beta-II tryptase;
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                GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp
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DB; AAS20765.
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CC producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a CC proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide CC at 1 tryptase. The active site mutants of proteolytic tryptase provide CC at 1 tryptase the structural and functional properties of the CC canstacase and its enzymatic activity, and for modelling studies. The CC enzymatically-active, recombinant proteolytic tryptase produced are CC useful as an antigen to generate anti-human tryptase antibodies CC antagonists, agonists, etc. The present sequence represents recombinant vy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to recombinant human proptases, active site mutants of these tryptases and
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCC 20

SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

CAGTGGGTGCTGACCGCCGCGGGGGGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 60 186

AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246

80

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ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 100

CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCTGCCTCA 366

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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active the mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The
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                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                            The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies
                                                                                                                                                                                                                                                                                                                      and in drug screening for compounds which act as tryptas antagonists, agonists, etc. AAU12009-AAU12024 represent human beta-II tryptase active site mutants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 93; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an active site mutation
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                                                               ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT
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                                                                due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies
                                                                                                                                                                tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity
                          and in drug screening for compounds which act antagonists, agonists, etc. AAU12009-AAU12024 human beta-II tryptase active site mutants.
                                                                                                                                                                                                                                                                                                                        DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase
Sequence
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enzyme;
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                                          AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG
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                                                                                                            construct for producing enzymptase, comprises DNA sequence active site mutation -
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 US-09-598-982-20 (1-771) x AAU12013 (1-245)
                                                                                                                                                                                   beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAUI2009-AAUI2024 represent recombinant
                                                                                                                                                                                                                                                                                    producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 40; Page 95-96; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation -
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                                                                                   LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer
                                                                                                                                     CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA
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                                     The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activit
due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase p
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                                                                                                                                                                                                                                                                                                                             CCGGGGATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
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                                                                                                                                                                     CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the deduced amino acid sequence of human mast cell tryptase II/beta (see also AAV44330). The invention provides: compositions comprising an isolated tryptase-7 that may include chimeric proteins that contain (a) a human tryptase for all but the active site region and (b) the substrate-binding pocket of mouse tryptase-7 or its homologues (see AAW64233-39); a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product, to decrease fibrinogen activity; a nucleic acid encoding a serine protease (5P); and a method of producing a mature SP by expressing the inactive zymogen in a host cell, and cleaving the enterokinase usceptibility domain. The tryptase-7 polypeptides can be used to treat disorders mediated by undesirable thrombus clot formation such as myocardial infarction and reocclusion following angioplasty of blood clots associated with pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, useful for all surgical procedures that require decreased blood
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                                                         CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG
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Search completed: January 31, 2003, 06:53:08 Job time : 59 secs

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-Q-/Ggn2_1/USPTO_Spool/US99598962/runat_27012003_073718_19634/app_query.fasta_1.967
-DB-Published_Applications_AA -QFMT-fastan -SUFFIX-n2p.rapb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS_bits -START=1 -END=-1 -MATRIX=DLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE—pct -THR_MXX=100
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-DEV_TIMEOUT=120 -WAARN_TIMEOUT=30 -THREADS=1 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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US-10-028-072-222
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Sequence 7, Appli
Sequence 222, App
                                                         Sequence 2, Appli
Sequence 115, App
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## ALIGNMENTS

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US-09-900-754-2
Sequence 2. Application US/09900754
Patent No. US20020086554A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING TRYPTASE GENE TITLE OF INVENTION: DISRUPTIONS
FILE REFERENCE: R-372
CURRENT APPLICATION NUMBER: US/09/900,754
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/216,109
PRIOR APPLICATION NUMBER: US 60/223,172
PRIOR APPLICATION NUMBER: US 60/223,172
PRIOR APPLICATION NUMBER: US 60/244,111
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-10-26
NUMBER: OF SEO ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 311
TYPE: PRT
ORGANISM: Mus musculus
US-09-900-754-2
Alignment Scores:
5.56e-33
Length: 311
Pred: No.:
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Best Local Similarity:
Query Match:
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Percent Similarity:
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSAMAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
                                                                                           GENERAL INFORMATION:
                                                                                                     Sequence 115, Application US/09888615 Patent No. US20020064856A1
                                                                             APPLICANT: PLOWMAN, GREGORY
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AsnTrpIleHisHisHisIleProGluAlaGlyGlySerGly
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Query Match:
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 115
LENGTH: 288
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Best Local Similarity:
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SEQ ID NO 7
LENGTH: 290
TYPE: PRT
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APPLICANT: Darrow, Andrew
APPLICANT: Diarrow, Andrew
APPLICANT: 0i, Jian-shen
TITLE OF INVENTION: DNA encoding the novel human
TITLE OF INVENTION: protease T
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 11
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CURRENT ADDITION:
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ORGANISM: Homo sapiens
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                            {\tt AsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyAspSer}
                                                 GACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGGGGACTCC:::|||||||||||||||
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                                                                                             {\tt LysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleLys}
                                                                                                                           ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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PRIOR APPLICATION NUMBER: 60/059113
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Godowski, Paul J.
Gurney, Austin L.
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Percent Similarity: Best Local Similarity:

4.89e-30 563.50 61.85% 44.18%

Length:
Matches:
Conservative:
Mismatches:

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Score:

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DR APPLICATION NUMBER: 60/069212
DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/069278
DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/06934
DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/06934
DR FILING DATE: 1997-12-16
DR APPLICATION NUMBER: 60/072320
DR FILING DATE: 1998-01-23
DR APPLICATION NUMBER: 60/073612
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/074086
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/07791
DR FILING DATE: 1998-03-20
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/079910
DR APPLICATION NUMBER: 60/079929
DR APPLICATION NUMBER: 60/07928
DR APPLICATION NUMBER: 60/07928
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/07928
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/08105
DR APPLICATION NUMBER: 60/081203
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/081203
DR FILING DATE: 1998-04-09
DR APPLICATION NUMBER: 60/081203
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RR APPLICATION NUMBER: 60/06
RR FILING DATE: 1997-11-24
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R APPLICATION NUMBER: 60/
R FILING DATE: 1997-11-03
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DB:
                 APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Darrow, Andrew
APPLICANT: Diar-shen
TITLE OF INVENTION: DNA encoding the novel h
TITLE OF INVENTION: Protease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/10/040,655
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020146805A1
GENERAL INFORMATION:
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US-10-041-006A-9
Sequence 9, Application US/10041006A
; Patent No. US/20020168754A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
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US-10-040-655-7
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TYPE: PRT
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LENGTH: 315
TYPE: PRT
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
                                                                                                                           IleLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGly
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FILE REFERENCE: ORT-1032

CURRENT APPLICATION NUMBER: US/10/040,655

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 315

TYPE: PATENT NUMBER: DIAMERITE NUMBER: PATENT NUMBER: US/10/040,655
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
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APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Q1, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
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ORGANISM: Homo sapiens
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APPLICANT: Darrow, Andrew
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
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APPLICANT: 0i, Jenson
TITLE OF INVENTION: DNA Encoding the Human
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
CURRENT FILING DATE: 2002-01-08
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SOFTWARE: PatentIn Ver. 2.0
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                               AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCC 126
                                                                 MetSerSerArgIleValGlyGlyArgAspGlyArgAspGlyGluTrpProTrpGlnAla
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TITLE OF INVENTION: DNA Encoding the Human Se:
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT 1031
CURRENT APPLICATION NUMBER: US/10/042,091A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEO ID NOS: 9
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  Query Match:
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                                                                                                                                                                                                                                                                                                         SEQ ID NO 7
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10041400A Patent No. US20020110895A1
                                                                                                        CURRENT APPLICATION NUMBER: US/10/041,400A CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                      APPLICANT: Andrade-Gordon, Patricia APPLICANT: Qi, Jenson TITLE OF INVENTION: DNA Encoding the TITLE OF INVENTION: Protease EOS
                                                                                                                                                                                                                                               APPLICANT: Darrow, APPLICANT: Andrada APPLICANT: Qi, Je
                                                    PRIOR APPLICATION NUMBER: US/09/387,375 PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                    FILE REFERENCE: ORT-1031
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                                   TyrSerProTrpIle
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; OTHER INFORMATION: ; OTHER INFORMATION: US-10-041-264A-9
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APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon
APPLICANT: Qi, Jenson
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ORGANISM: Artificial Sequence
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                              GTCCGTGACGACATGCTGTGTGCCGGG-----AACACCCGGAGGGACTCATGCCAGGGC
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TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/042,091A
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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                                                          ArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAlaLeu
                                                                                         AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
                                                                                                                     ValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValProVal
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GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, In:
APPLICANT: Mok, Samuel
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer;
FILE REFERENCE: 81994/282423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity:
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LENGTH: 343
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ORGANISM: Homo
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publication No. US20020197701A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides,
FILE REFERENCE: PT005P4
CURRENT APPLICATION NUMBER: US/10/067,761
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                               SOFTWARE: PatentIn
SEQ ID NO 19
LENGTH: 238
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                                                                            CysArgAsp------TyrProGlyProGlyGlySerIleLeuGlnPro
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                                                            LeuValCysGlnValAsnGlyAlaTrpValGlnAlaGlyThrValSerTrpGlyGluGly
                                                                                                                         AspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSerGlyGlyPro
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-Q=/ggn2_1/USPTO_spool/US09598982/runat_27012003_073717_19581/app_query.fasta_1.967
-DB=PIR_73 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09598982_GCGN_1 1_15_@runat_27012003_073717_19581 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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## ALIGNMENTS

A;Note: reserver 1.S.; Moxley, G.; Schwartz, L.D.
R;Miller, J.S.; Moxley, G.; Schwartz, L.D.
J. Clin. Invest. 86, 864-870, 1990
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptas tryptase (EC 3.4.21.59) II precursor - human
N;Alternate names: tryptase beta
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #Sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000
C;Accession: B35863; A37193; I59473
C;Accession: B35863; A37193; I59473 Scand. J. Immunol. 37, 203-208, 1993
A;Title: Characterization of a tryptase mRNA expressed in the human basophil cell lin A;Reference number: 159473; MUID:93166209; PMID:8434231
A;Accession: 159473
A;Status: preliminary; translated from GB/EMBL/DDBJ R; Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A; Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A; Reference number: A35863; MUID:90251647; PMID:2187193
A; Accession: B35863 R;Blom, A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584 A; Molecule type: mRNA A; Residues: 1-275 <MIL> A;Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983 A;Note: residues 2-275 are derived from mRNA; residue one was inferred f R;Miller, J.S.; Moxley, G.; Schwartz, L.B. A; Molecule type: mRNA; DNA A; Residues: 1-275 < VAN> T.; Hellman, ÷ from the genom

KFHU1

coagulation

factor

A;Cross-references: GB:S55551; NID:g265666; PIDN:AAD13876.1; A;Experimental source: basophil cell line KU812 C;Genetics:

PID:g4261576

A; Molecule type: mRNA A; Residues: 1-275 < RES>

A;Gene: GDB:TPS1
A;Cross-references: GDB:125890;

OMIM:191080

position: 16pter-16qter

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Alignment
Pred. No.:
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C;Keywords: hydrolase; serine proteinase; zymogen
E;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted </F;31-275/Product: tryptase I #status predicted <MAT>
E;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predict
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A; Molecule type: DNA
A; Residues: 1-275 <VAN>
A; Cross-references: GB:M33494; NID:g3927804; PIDN
A; Accession: D33863
A; Molecule type: mRNA
A; Residues: 1-275 <VA2>
A; Cross-references: GB:M33491
A; Cross-reference no cf: Weiler, D.A.; Hunt, L.W.; Wy
J. Leukoc. Biol. 47, 409-419, 1990
A; Title: Purification of tryptase from a human man
A; Reference number: A60939; MUID:90244210; PMID:2
A; Accession: A60939
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
E;1-21/Domain: signal sequence #status predicted <SIG>
E;22-30/Domain: activation peptide #status predicted <AC
E;31-275/Product: tryptase I #status experimental <MAT>
E;31-275/Domain: trypsin homology <TRY>
E;31-275/Domain: Hydrolase I #status predicted *AC
E;31-275/Domain: Trypsin homology <TRY>
C;31-275/Domain: Try
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A; Molecule type: protein
A; Residues: 31-38, 'p', 40-41,'X', 43,'T', 45-48,'X',50 <BUT>
A; Experimental source: mast cell
A; Note: 44-6ly was also found
R; Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Jo
J. Biol. Chem. 262, 1363-1373, 1987
A; Title: Human pituitary tryptase: molecular forms, NH-2-terminal
A; Reference number: A39326; MUID:87109258; PMID:3543004
A; Accession: A39326
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C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C:Accession: A35863; D35863; A60939; A39326
R:VanderSlice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multige A; Reference number: A35863; MUID:90251647; PMID:2187193
A; Accession: A35863;
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A;Residues: 31-38 <CRO>
A;Experimental source: pituitary
C;Genetics:
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submitted to GenBank, April 1990
A; Reference number: A38893
A; Reference number: A38893
A; Reference number: A38893
A; Recession: A38893
A; Molecule type: mRNA
A; Residues: 9-131, 'K',132-275 <VA3>
A; Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-30/Domain: activation peptide #status predicted <ACT>F;31-27/Product: tryptase I #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
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A;Title: Human mast cell tryptase: multiple cDNAs and genes A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: C35863
                              Query
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A; Residues: 1-9 < VA2>
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A; Residues: 9-275 < VAN>
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C:Species: Homo sapiens (man)
C:Accession: A45754; B37193
R:Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A;Title: Cloning and characterization of complementary DNA
A;Reference number: A45754; MUID:90009311; PMID:2677049
A;Accession: A45754
       A; Molecule type: mRNA
A; Residues: 1-274 < MIL>
A; Residues: 1-274 < MIL>
A; Cross-references: GB: M30038
A; Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A; Title: Cloning and characterization of a
A; Reference number: A37193; MUID:90369005;
A; Accession: B37193
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Transcription

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A;Cross-references: GB:M30038
A;Ote: the sequence from Fig. 4 is inconsistent with that from C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-30/Domain: activation peptide #status predicted <ACT>F;31-274/Product: tryptase I #status predicted <AACT>F;31-274/Product: tryptase I #status predicted <AACT>F;31-274/Product: trypsin homology <TRY>
F;31-266/Domain: trypsin homology <TRY>
F;74,120,223/Active site: His, Asp, Ser #status predicted
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     ValProLysLysPro
                                                           GTCCCCAAAAAGCCG
                                                                                                             ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr
                                                                                                                                                                CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT
                                                                                                                                                                                                                      {\tt CysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgValue}
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C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted ACT>
F;32-276/Product: mast cell proteinase 6 #status experimental
F;33-268/Jomain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change C;Accession: A38654; B38654; D35646; I59478 R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E. J. Biol. Chem. 266, 3847-383, 1991 A;Title: Cloning of the cDNA and gene of mouse mast cell proteas A;Reference number: A38654; MUID:91139682; PMID:1995638 A;Accession: A38654
                                                                                                                                                           Qy
                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 32-54 < RE3>
R; Huang, R; Abrink, M; Gobl, A.E.; Nilsson
R; Huang, R; Abrink, M; Gobl, Coll typtase
A; Title: Expression of a mast cell tryptase
A; Reference number: 159478; MUID:94023807; P
A; Accession: 159478
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Best Local Similarity:
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A; Residues: 1-276 < RES>
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A; Residues: 1-276 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-598-982-20 (1-771) x A38654 (1-276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: MMCP-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
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A; Residues: 1-276 < REY>
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                                                     GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG
GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104
                                                                                                                                                             ATCCACCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG
                                                                                                     {\tt TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuArgPheLysLeuA
                                                                                                                                                                                                                                                                                                                        {\tt ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpProperties} \\
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<MAT>

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tryptise (EC 3.4.21.59) precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
C:Accession: A32410
R:Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A:Title: Molecular cloning of dog mast cell tryptase and a related protease: str
A:Reference number: A32410; MUID:89352460; pMID:2504277
A:Reference number: A32410; MUID:89352460; pMID:2504277
A:Residues: 1-275 <VAN>
A:Residues: 1-275 <VAN>
A:Residues: 1-275 <VAN>
A:Residues: 1-275 <VAN>
C:Superfamily: trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-25/Product: tryptase #status predicted <ACT>
F:31-25/Product: tryptase #status predicted <ACT>
F:31-24/Active site: His, Asp, Ser #status predicted
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                                                                                                                               A;Cross-references: EMBL:D31789; NID:g517122; C;Superfamily: trypsin; trypsin homology F;26-262/Domain: trypsin homology <TRY>
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Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A; Title: Isolation, characterization, and transcription
A; Reference number: A47246; MUID:93087489; PMID:1454796
A; Reference number: A47246
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A;Cross references: GB:L00653; NID:g200518; PIDN:AAA39992.1; A;Note: sequence extracted from NCBI backbone (NCBIN:119745, C:Superfamily: trypsin; trypsin homology C:Keywords: hydrolase; serine proteinase F;29-265/Domain: trypsin homology <TRY>
                                                                                                                                                       tryptase (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47246
R;McNell, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Av
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
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A; Residues: 1-273 <MCN>
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tryptase (EC 3.4.21.59) precursor - rat N;Alternate names: mast cell tryptase C;Species: Rattus norvegicus (Norway rat) C;Date: 27-Aug-195 #sequence_revision 27-OC C;Accession: JC4171 R;Ide, H.; Itoh, H.; Tomita, M.; Murakumo, Y J. Biochem. 118, 210-215, 1995 A;Title: cDNA sequencing and expression of r
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A;Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID: C:Comment: This enzyme is basically specific for a connective tissu einase inhibitors.
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; F:1-19/Domain: signal sequence #status predicted <SIG> F:1-19/Domain: signal sequence #status predicted <ACT> F:20-29/Domain: activation perpide #status predicted <AMAT> F:30-214/Product: mast cell tryptase #status predicted <MAT> F:73.120.223/Active site: His, Asp. Ser #status predicted
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A; Accession: JC4171
A; Molecule type: mRNA
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A;Residues: 'IVGGQEAP',1=8;61-74;90-97;126-148;162-190;208-222;227-235
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein: hydrolase; serine proteinase; zymogen
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C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: S68702; S68676
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DB:
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A; Residues: 1-237 < PAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: cDNA cloning and primary structure of tryptase A; Reference number: S68676; MUID:96203914; PMID:8620861
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Best Local Similarity:
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A;Cross-references: EMBL:X78542; NID:g468809; C;Superfamily: trypsin; trypsin; homology C;Keywords: hydrolase; serine proteinase E;32-230/Domain: trypsin homology #status atyp
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A;Molecule type: mRNA
A;Residues: 1-230 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 40, 397-414, 1994
A;Title: Genes for mast-cell serine protease and their molecular
A;Reference number: I48684; MUID:95048582; PMID:7959952
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GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCTGCCG
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                                                                                    GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer
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Conservative:
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Biochemistry 28, 4148-4155, 1989

A; Title: Molecular cloning of dog mast cell tryptase and a ray Reference number: A32410; MUID:89352460; PMID:2504277

A; Reference number: A32410; MUID:89352460; PMID:2504277

A; Rocession: B33410

A; Molecule type: mRNA

A; Residues: 1-269 < VAN>

A; Cross-references: GB:M24665; NID:g163984; PID:g163985; GB:A; Cross-references: GB:M24665; NID:g163984; PID:g163985; GB:A; Note: the authors translated the codon ACG for residue 114
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-19/Domain: signal sequence #status predicted < F; 20-259/Domain: trypsin homology < TRY>
F; 66,116,217/Active site: His, Asp, Ser #status predicted
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                               AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAA 480
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prostasin | C;Species: C;Date: 24-C;Accession
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A;Map position: 16p11.2-16p11.2
C;Superfamily: prostasin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane prot
F;1-32/Domain: signal sequence #status predicted <SIO>F;1-32/Domain: prostasin in #status predicted <CHL>F;3-44/Domain: prostasin light chain #status predicted <CHL>F;3-44/Domain: prostasin heavy chain #status predicted <CHH>F;3-23-34/Domain: transmembrane #status predicted <CHH>F;45-343/Domain: transmembrane #status predicted <CHH>F;5-281/Domain: transmembrane #status predicted <MIMI>F;37-154,70-86;168-244,201-223,234-262/Disulfide bonds: #status predicted
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J. Biol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine proteinase from seminal f. A;Reference number: A54866; MUID:94308140; PMID:8034638
A;Accession: A54866
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J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific expression, and A;Reference number: A57014, MUID:95286644; PMID:7768952
A;Accession: A57014
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A; Residues: 1-343 < RES>
                                                                                                         US-09-598-982-20 (1-771) x A57014 (1-343)
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                                                                                                                                                                                                                 Best Local Similarity:
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Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
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                                                                      A;Cross-references: GB:M18295
A;Note: the sequence shown follows the authors' t
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; E
Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI,
A;Reference number: A00920; MUID:86243360; PMID:3
A;Recession: A00920
                                                                                                                                                                                                                                                                                                                                                                                    coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human N;Alternate names: antihemophilic factor C; plasma thromboplastin ar C;Species: Homo sapiens (man) C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-IC;Accession: A27431; A00920; A37940 R;Asakai, R.; Davie, E.W.; Chung, D.W. Biochemistry 26, 7221-7228, 1987
                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-625 < ASA>
                                                                                                                                                                                                                                                                                                             A; Title: Organization of the gene for human factor XI. A; Reference number: A27431; MUID:88107663; PMID:2827746 A; Accession: A27431
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A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1;
                        A; Molecule type: mRNA
A; Residues: 1-625 < FUJ>
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PMID:3636155
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A; Description: catalyzes the proteolytic activation of coagulation factor IX
A; Pathway: blood coagulation intrinsic pathway
C; Superfamily: coagulation factor XI; trypsin homology
C; Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
F; 19-18/Domain: signal sequence *status predicted <SIG>
F; 19-18/Domain: appla repeat <AP1>
F; 19-198/Domain: apple repeat <AP2>
F; 199-198/Domain: apple repeat <AP2>
F; 199-288/Domain: apple repeat <AP2>
F; 199-288/Domain: apple repeat <AP4>
F; 388-632/Product: coagulation factor XIa light chain *status experimental <LCH>
F; 388-632/Product: coagulation factor XIa light chain *status experimental <LCH>
F; 388-638/Domain: trypsin homology <TRK'>
F; 383-618/Domain: trypsin homology <TRK'>
F; 385-638/Domain: trypsin homolo
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A; Map position: 4q35-4q35
A: Introns: 19/1; 73/2; 10
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Biochemistry 30, 2056-2060, 1991
A;Title: Location of the disulfi
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Best Local Similarity:
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          CTGCTGGAGCTGGAGGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC
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                                                                                                   LeuLeuLysLeuGluThrThrValAsnTyrThrAspSerGlnArgProIleCysLeuPro
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A; Map position: 4q35-4q35
A; Map position: 4q35-4q35
C; Superfamily: coagulation factor XI; trypsin home C; Keywords: blood coagulation; duplication; fibrif; 17-19/Domain: signal sequence #status predicted F; 1-19/Domain: signal sequence #status predicted F; 20-638/Product: plasma kallikrein #status predicted F; 20-638/Product: plasma kallikrein heavy chain #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein

A;Residues: 20-27;40-46', X', 48, 'H';50, 'X', 52-70', 'H';75-76, 'X', 78-80;103-113;131-140;1

A;Residues: 20-27;40-46', X', 293-295;314-317, 'X', 319-320;321-324; 'X', 329-333;334-339,

26:0-283, 'X', 285;287-291, 'X', 293-295;314-317, 'X', 319-320;321-324; 'X', 329-333;334-339,

25:538-551;562, 'X', 564-567;573, 'X', 575-576;578-583, 'X', 585;592-604 <mc/>
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent comple
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a

are linked by one or more disulfide bonds.

C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciproca

lingen and may also play a role in the renin-angiotensin system by converting proreni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma kallikrein (EC 3.4.21.34) precursor - human kallikrein (EC s.4.21.34) precursor - human kallikrein plasma prekallikrein (FC s.5 pecies: Homo sapiens (man) C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 C:Accession: A00921; A37939
F:110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP3>
F;391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;391-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,F;217-308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimenta F;318-347,340-345/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Human plasma prekallikrein, a zymogen to a serine A;Reference number: A00921; MUID:86243359; PMID:3521732 A;Accession: A00921
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                                                                                                                                                                                                                                                                           F;20-390/Domain: plasma kallikrein heavy
F;20-109/Domain: apple repeat <AP1>
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Search completed: January 31, Job time: 33.5 secs
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                                                                                                                                                                                                                     GlnAspTyrLysIleThrGln---ArgMetValCysAlaGlyTyrLysGluGlyGlyLys
                                                                                                                                                                                                                                                                           IleProLeuValThrAsnGluGluCysGlnLysArgTyr-----
                                                                                                                                                                                                                                                                                                                                   LysGlyGluIleGlnAsn-----------------IleLeuGlnLysValAsn 539
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GlyAspThrSerThr1leTyrThrAsnCysTrpValThrGlyTrpGlyPheSerLysGlu
                                                    ThrLysValAlaGluTyrMetAspTrpIle 621
                                                                    ACCCGTGTCACCTACTTGGACTGGATC 729
                                                                                                          {\tt AspAlaCysLysGlyAspSerGlyGlyProLeuValCysLysHisAsnGlyMetTrpArg}
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

a		Result No.
110 111 113 114 115 116 117	, , , , , , , , , , , , , , , , , , ,	ult No.
187.8 187.6 187.6 1184.4 1184.2 1181.2 1181.2 1181.2 1180.4 1180.4	201.4 201.4 201.4 201.4 193.8 193.8 191.6	Score 726.2
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Query Match 94.2%; Best Local Similarity 98.3%; Matches 734; Conservative

Score 726.2; DB 10; Pred. No. 7.4e-162; 0; Mismatches 13;

Indels

0;

Gaps

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Length 1081;

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## ALIGNMENTS

RESULT 1 US-09-954-456-2126

Sequence 2126, Application US/09954456 Patent No. US20020115057A1

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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR PPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,537
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,731
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PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,86
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying An
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,052
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PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                      US-09-954-456-2242/c

: Sequence 2242, Application US/09954456

: Patent No. US20020115057A1
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                                                                                           APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jian-shen
TITLE OF INVENTION: DNA encoding the novel h
TITLE OF INVENTION: protease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/10/041,006A
CURRENT EILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                        RESULT 3
US-10-041-006A-1
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                  ; TYPE: DNA
; ORGANISM: Homo
US-10-041-006A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: n=a,t,g
US-09-954-456-2242
                                                                                                                                                                                                                Sequence 1, Application US/10041006A Patent No. US20020168754A1 GENERAL INFORMATION:
                                                    SOFTWARE: PatentIn
SEQ ID NO 1
LENGTH: 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 286; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo
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NAME/KEY: misc_feature
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PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR TILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2242
LENGTH: 616
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GGACTCATGCCAGGGCG-ACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGC
                                            ACACCCGTGTCACCTACTTGGACTGGATCCACCACTATGTCCCCCAAAAAGCCGTGAA
                                                                                       GGACTCATGCCAGGGCGAACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGC
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26.1%; 57.4%;

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APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: O1, Jian-shen
TITLE OF INVENTION: DNA encoding the novel b
TITLE OF INVENTION: DNA encoding the novel 
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Pred. No. 1.2e-38;
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Sequence 221, Application No. US200:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Kev
APPLICANT: Beresini
APPLICANT: DeScoyer;
APPLICANT: Filvarof;
APPLICANT: Gao, Wei-(

Baker, Kevin P.

Application US/10028072 o. US20030004311A1

Gao, Wei-Qiang Desnoyers, Luc Filvaroff, Ellen DeForge, Laura Beresini, Maureen RESULT 5 US-10-028-072-221

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; LENGTH: 1110
; TYPE: DNA
; ORGANISM: HO
US-10-040-655-1
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mes 433; Conserv
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CAACTGGATCCATCGGATCATCCCCAAACTGCAGT
              GGACTGGATCCACCACTATGTCCCCAAAAAAGCCGT
                                                                                                                 TGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGACTC
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Pred. No. 1.2e-38;
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TITLE OF INVENTION:

FILE REFERENCE:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059115

PRIOR APPLICATION NUMBER: 60/059115
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OR FILING DATE: 1997-10-17
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062816
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-27
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063550
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063755
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DR APPLICATION NUMBER: 60/059115
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059117
DR FILING DATE: 1997-09-17
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059122
DR APPLICATION NUMBER: 60/059124
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059184
DR FILING DATE: 1997-09-17
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PR APPLICATION NUMBER: 60/059352

PR FILING DATE: 1997-09-19

PR APPLICATION NUMBER: 60/059588

PR FILING DATE: 1997-09-19

PR APPLICATION NUMBER: 60/059836

PR APPLICATION NUMBER: 60/06250

PR APPLICATION NUMBER: 60/062250

PR FILING DATE: 1997-10-17

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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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NUMBER:

1998-05-

60/085704 60/085697

APPLICATION NUMBER: 60/086414 FILING DATE: 1998-05-22

FILING DATE: 1998-05-1 APPLICATION NUMBER:

APPLICATION NUMBER: 60/086430

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APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
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FILING DATE: 19/98-06-11
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTC
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Pred. No. 1.2e-38;
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                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8
LENGTH: 1130
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: protease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/10/041,006A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Andrade-Gordon,
APPLICANT: Darrow, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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328
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CTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGC
                                                         TGGGTCCTGACGCCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTC
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Pred. No. 7.5e-37;
0; Mismatches 307;
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                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                  SEQ ID NO 8
LENGTH: 1130
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Darrow, Andrew APPLICANT: Q1, Jian-shen TITLE OF INVENTION: DAA encoding the TITLE OF INVENTION: protease TITLE REFERENCE: ORT-1032
                                                                                                                                                                              -10-040-655-8
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/040,655
CURRENT FILLING DATE: 2002-01-07
NUMBER OF SEO ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andrade-Gordon,
                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                           CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
                                                         GATGACAAGATCGTTGGGGGCTATGCTCTAGAGGAGGGCGAGTGGCCCTGGCAAGTCAGC
                                                                                                                   Conservative
-CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAG
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56.7%;
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                                                                                                                                 Score 193.8; DB 1
Pred. No. 7.5e-37;
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; SOFTWARE: PatentIn Ver. 2; SEQ ID NO 35; LENGTH: 2847; TYPE: DNA; ORGANISM: Homo sapiens US-09-888-615-35
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APPLICANT: WHYTE, DAVID
APPLICANT: CHENEPEL, SEN
APPLICANT: CHARYDCZEK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: MOVEL PROTEASES
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application UPatent No. US20020064856A1
Query Match
Best Local
                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
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Pred.
 191.6; DB
No. 3e-36;
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Similarity

Matches

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                                                                     US-10-041-400A-1
                                                                                                                       PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
FEBOURD 1.00
    Query Match 24.4
Best Local Similarity 56.9
Matches 414; Conservative
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10041400A Patent No. US20020110895A1
                                                                                                                                                                                                         APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Q1, Jenson
TITLE OF INVENTION: DNA Encoding the Human
FITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                                          APPLICANT: Darrow,
                                                                               LENGTH: 1613
TYPE: DNA
ORGANISM: Homo sapiens
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 Score 187.8; DB 12;
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0; Mismatches 292;
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CURRENT APPLICATION NUMBER: US/10/041,264A CURRENT FILING DATE: 2002-01-08 PRIOR APPLICATION NUMBER: US/09/387,375 PRIOR FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 1613
                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                       Sequence 1, Application US/10041264A Patent No. US20020142446A1
                                                                                                                          APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patri
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
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; TYPE: DNA ; ORGANISM: Homo sapiens US-10-041-264A-1
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          GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
                                                                                             Sequence 1, Application US/10042091A Patent No. US20020142447A1
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NUMBER: US/10/042,091A
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; LENGTH: 1613
; TYPE: DNA
; ORGANISM: Homo :
US-10-042-091A-1
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Matches 414; Conserv
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Best Local
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SOFTWARE: PatentIn Ver. 2.0
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PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
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             GGATCCA
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                                                                  AGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACT
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GGATTCA
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Pred. No. 2.1e-35;
0; Mismatches 292;
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RESULT 12
US-09-900-754-1
; Sequence 1, Application US/09900754
; Patent No. US20020026654A1
; GENERAL INFORMATION:

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CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/216,109
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: US 60/223,172
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 60/244,111
PRIOR APPLICATION NUMBER: US 60/244,111
PRIOR FILING DATE: 2000-10-26
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LENGTH: 1122
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: DISRUPTIONS
FILE REFERENCE: R-372
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APPLICANT: Leviten, Micha
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ORGANISM: Mus musculus
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                   CCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACC
                                                                                                                                                                                                         TCCCACCGCCATTTCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTG
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GCCGCCCTGACCGCCCTGGCGTCTATGCCCGGGTTACTGCCTATGTAAACTGGATCCACC
                                                                  TCTGCCAGGTGGCTGGAACCTGGCAGCAGGCCGGCGTTGTCAGCTGGGGTGAGGGCTGTG
                                                                                    TGTGCAAGGTGAATGGCACCTGGCTGGCGGGCGGGCGTGGTCAGCTGGGGCCAGGGCTGTG
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                                                                                                                                      TGCTATGCGCCCGGGGCCCTG----GGGATGCCTGCCAGGATGACTCTGGAGGGCCACTAG
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Sequence 8, Application US/10041400A
Patent NO. US20020110895A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson Encoding the Human Se
TITLE OF INVENTION: DNA Encoding the Human Se
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT 1031
CURRENT APPLICATION UNMEER: US/10/041,400A
CURRENT FILING DATE: 2002-01-08
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; OTHER INFORMATION: Clone ID: 07-LIB188-011-Q1-E1-B11
US-09-960-352-1410
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US-09-960-352-1410/c
Sequence 1410, Application
Patent No. US20020137139A1
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                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1130
TYPE: DNA
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LENGTH: 249
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APPLICANT: Warren, Wesley
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Best Local Similarity
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
                                                                                   PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Artificial Sequence
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RESULT 15
US-10-041-264A-8
: Sequence 8, Application US/10041264A
: Patent NO. US20020142446A1
: GENERAL INFORMATION:
; APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Se
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
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; OTHER INFORMATION:
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US-10-041-400A-8
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                                                                                                                                Andrade-Gordon, Patricia
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-041-264A-8
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LENGTH: 1130
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Best Local
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SOFTWARE: PatentIn Ver
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                                                                                                                    AGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGC
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                                                   CCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCCTGGATTCAGGCTCGCG
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Pred. No. 6.8e-34;
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Maximum DB
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                 Score
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length: 2000000000
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1: /cgn2_6/ptodata/l,
2: /cgn2_6/ptodata/l,
3: /cgn2_6/ptodata/l,
4: /cgn2_6/ptodata/l,
5: /cgn2_6/ptodata/l,
6: /cgn2_6/ptodata/l,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
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DB
             US-09-079-970A-4
US-08-978-404B-13
US-08-978-404B-13
US-09-016-366A-28
US-09-016-366A-21
US-09-016-366A-21
US-09-016-366A-21
US-09-016-366A-21
US-09-016-366A-21
US-08-978-404B-11
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-08-978-404B-1
US-09-016-366A-24
US-08-978-404B-1
US-09-430-854-5
US-09-430-854-5
US-09-430-854-5
US-09-386-653A-1
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US-09-386-653A-1
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Million cell updates/sec
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                            20, Appli 18, Appli 18, Appli 19, Appli 17, Appli 18, Appli 18, Appli 19, Ap
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45	44	43	42	41	40	39	38	37	36	S	34	33	32	31	30	29	28
	95.6		98.4	100.8	102.8	103.6	103.6	107.6	108.6	112.8	115.4		129.2		140.6	140.6	143.8
12.2	12.4	12.4	12.8	13.1	13.3	13.4	13.4	14.0	14.1	14.6	15.0	15.0	16.8	17.0	18.2	18.2	18.7
1387	1240	1155	2544	654	2416	1755	1386	1109	1109	2413	1103	1081	1166	1430	1169	1142	2397
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5270178-1	US-09-163-951-14	US-09-163-951-15	US-09-518-046-3	US-09-280-116-57	US-09-261-416-1	5225537-1	US-08-756-506-3	US-09-088-651-1	US-09-088-651-6	US-09-518-046-1	US-09-386-642-59	US-09-008-271A-15	US-09-386-629-2	US-09-386-629-1	US-09-386-642-7	US-09-386-642-8	US-08-978-404B-2
Patent No. 5270178	Sequence 14, Appl	Sequence 15, Appl	Sequence 3, Appli	Sequence 57, Appl	Sequence 1, Appli	Patent No. 5225537	Sequence 3, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 59, Appl	Sequence 15, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-09-079-970A-4
                                                                                                                                                                                                          TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09079970A
Patent No. 6274366
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 3450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
                                                                                                                                       HYPOTHETICAL: N
                                                                                                                                                     TOPOLUGE: DN MOLECULE TYPE: DN
                    LOCATION: FEATURE:
                                                                           ORGANISM: FEATURE:
                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
NAME/KEY: misc_signal
                                                           NAME/KEY:
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                                    CDS
7..753
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                                                                                                 Sequence 20 Patent No.
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                                                                                         GENERAL INFORMATION:
                                          APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL!
TITLE OF INVENTION: INHIBITORS
                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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STREET: 60
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                                                                                                  20, Application US/09016366A
5. 5955431
E: Wolf, Greenfield 600 Atlantic Avenue
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99.5%;
                                                       MAST CELL PROTEASE
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Pred. No. 1.4e-164;
0; Mismatches 4;
           Sacks,
                                                       PEPTIDE
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Best Local Similarity
Matches 737; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
COUNTRY: U.S.
ZIP: 02210-22
COMPUTER READABL
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/037,090 FILING DATE: 05-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
CCCCGGGGATGCCGTGCTGGGTCACTGGGTGGGCGATGTGGACAATGATGAGCGCCTCC
                                                                                                                                                                                                                  CGGTGAAGGTCTCCAGCCACACGGTCACACGCTCACCCTGCCCTCAGAGACCCTTCC
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                                                                CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAAAACCACATTTGTGACG
                                                                                                                                 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC
                                                                                                                                                                                                CGGTGAAGGTCTCCAGCGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCC
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TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.
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98.7%;
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Pred. No. 6e-157;
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RESULT 3
US-08-978-404B-15
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                                                                                 Query Match
Best Local S
Matches 737
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                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stevens, TITLE OF INVENTION:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B08
RELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
COUNTRY: U.S.
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                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                   NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                     77
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                                                                                 Local Similarity
mes 737; Conserv
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                                        ATGTCCCCAAAAAGCCGTGAGTCAGGC
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                                                           GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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o. 5968782
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02210-2211
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WENTION: MAST CELL PROTEASE
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                          94.8%;
98.7%;
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                                                                               Score 731; DB 2;
Pred. No. 6e-157;
0; Mismatches 10
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RESULT 4
US-09-016-366A-18
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              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for WI
CURRENT APPLICATION NUMBER: US/O
FILING DATE: January 30,
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stevens, Rich APPLICANT: Huang, Chifu
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  STREET: 600 Atla
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
                                                                                                                                                                                 COMPUTER:
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APPLICATION NUMBER:
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                                                                                                                                    FastSEQ for Windows Version
                                                                                                                                                                               IBM Compatible
                                                              January 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard L.
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Y 30, 1998
60/037,090
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SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
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cal Similarity 98.7%;
737; Conservation
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                                                          TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT
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ATGTCCCCAAAAAGCCGTGAGTCAGGC
              ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
                                                                                                                                                         GCAAGGTGAATGGCACCTGGCTGCAGGCGGGGGGGTGGTCAGCTGGGGGGGAGGGCTGTGCCC
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                                                                                         AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
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 Mismatches

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US-08-978-404B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-DEC-1996
ATTORNEY_AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE / TO THE PLANTAGE AND TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
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ADDRESSEE: Wolf, Greenfield &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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CITY: E
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Local Similarity 98.7%;
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                           CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCC
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US-09-079-970A-1
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                                                                                                                 NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 3450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09079970A
Patent No. 6274366
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone TISSON T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
COMPUTER: IBM PC COMPOUTER: IBM PC COMPOUTER: GYSTEM: PC.
SOFTWARE: Patentin Rei
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APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
            MOLECULE TYPE: HYPOTHETICAL:
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
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CITY: Madison
STATE: WISCONS
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                                           LENGTH: 735 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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RESULT 7 US-09-016-366A-22

Sequence 22, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: INHIBITORS

PROTEASE PEPTIDE

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                                                                                                                                                                                                                                                    CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
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GTCCCCAAAAAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGTCGGGGGTCAGGAGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC
            GTCCCCAAAAAGCCG
                                                                                          TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
                                                                                                                                                     TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
                                                                                                                                                                                        AAATACCACCTTGGCGCCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG
                                                                                                                                                                                                    AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG
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                                                                                                                   AAGGTGAATGGCACCTGGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG
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Pred. No. 1.9e-156;
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NUMBER OF SEQUENCES:

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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
-016-366A-22
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STREET: 600 A
CITY: Boston
STATE: MA
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TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCCGGTCCAGCAGGATCATCGTGC 256
                                                                                                                                                                                                                                                                                                                                       TGACCGCCGCGCGTGCGTGCGACCGCCGCACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
                                                                                            CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGGGGGATGTGGACAATGATGAGCGCCTCC 436
                                                                                                                             ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
                                                                                                                                                                                                                                                                                                                                                                                       TCCGCGACCGATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 185
                                                                                                                                                                                                                                                                                                                                                                                                      TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATCGTTGGGGGTCAGGAGGCCCCCCAGGAGCAAGTTGGCCCTTGGCAGGTGAGCCTTGAGAG 125
                                                              CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCGGCCTCAGAGACCTTCC 376
                                                                                                                                                                                                                                                                                                                      TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
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                                                                                                                                                                                              ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC
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02210-2211
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Pred. No. 7.2e-156;
0; Mismatches 13;
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TOPOLOGY:
US-08-978-404B-17
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                                                      Query Match
Best Local S
Matches 734
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GENERAL INFORMATION:
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
EILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wolf, Greenfield &
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                                                                                                                                                                                                                                                             NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63 REFERENCE/DOCKET NUMBER: E
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02210-2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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                                                       Local Similarity les 734; Conser
                                                                                                                                     STRANDEDNESS: single
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GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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                                                       Conservative
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MAST CELL PROTEASE THAT CLEAVES
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                                                                  Score 726.2;
Pred. No. 7.
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Mismatches
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                                                      2; DB 2;
7.2e-156;
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US-09-016-366A-16
                                                                                                                                                                                                                                                                                                             Sequence 16, Application Patent No. 5955431 GENERAL INFORMATION:
          ADDRESSEE: Wolf, Green STREET: 600 Atlantic and Color State: MA COUNTRY: Boston STATE: MA COUNTRY: U.S.A. ZIP: 02210-2211 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATING SYSTEM: DOS SOFTWARE: FASTSEQ FOR CURRENT APPLICATION DATA COURSES.
                                                                                                                                                                                             NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
                                                                                                                                                                                                                                               TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                APPLICANT: Stevens, Richard APPLICANT: Huang, Chifu
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             ARE: FastSEQ for Windows APPLICATION DATA:
                                                                                                                                                                            600 Atlantic Avenue
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NUMBER:
                                                                                Diskette
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Best Local Sim:
Matches 712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 712; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/032,354 FILING DATE: 04-DEC-1996 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: Wolf, Greenfield &
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1154 base pairs
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                                                                          TGCGGGAGCAGCACCTCTACCTACCAGGACCAGCTGCCGGTCAGCAGGATCATCGTGC
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ACCCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC
                                                         TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCAGTCAGCAGGATCATCGTGC
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VENTION: MAST CELL PROTEASE THAT CLEAVES

VENTION: FIBRINOGEN
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                                                                                                                                                                                                                                                                                                Score 686.2; DB 2;
Pred. No. 8.2e-147;
0; Mismatches 43;
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                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
EILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 60/032,354
EILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REGISTRATION NUMBER: 36,637
                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
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SEQUENCE CHARACTERISTICS:
LENGTH: 1219 base pair
                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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CITY: Boston
STATE: MA
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                                                       TELEX:
                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wolf, Greenieuu STREET: 600 Atlantic Avenue
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1219 base pairs
                                                                     617-720-2441
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MAST CELL PROTEASE THAT CLEAVES
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; TOPOLOGY:
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                                                                                     Sequence 14, Application US/09016366A Patent No. 5955431
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Best Local
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                                                                         GENERAL INFORMATION:
                       APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE
TITLE OF INVENTION: INHIBITORS
CORRESPONDENCE ADDRESS:
             NUMBER OF SEQUENCES:
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STRANDEDNESS: sing
TOPOLOGY: linear
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Pred. No. 1.6e-99;
0; Mismatches 173
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                                    PEPTIDE
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Best Local Sim
Matches 571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CITY: Boston
STATE: MA
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1108 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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CAAAATACCACCTTGGCGCCTACACGGGAGGACGTCCGCCATCGTCGTCGACGACATGC
                                                                                                                                                            CTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCTGCCTCGGAGACCTTCC
                                                                         CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG
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                                            CACCTCCTTATCCTCTGAAGCAAGTGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACC
                                                                                                     CCCCTGGGACATCGTGCTGGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCC
                                                                                                                     CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC
                                                                                                                                                                                         CGGTGAAGGTCTCCAGGCCACGTCCACACGGTCACCCTGCCCTGCCTCAGAGACCTTCC
                                                                                                                                                                                                                     ACCCACAGTTCTACACCGCCCAGATCGGAGGGGACATCGCCCTGCTGGAGGTGGAGGAGC
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: January 30, 1998
'ON: 530
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Pred. No. 8.1e-98;
); Mismatches 169;
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US-08-978-404B-20
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                                                                                                                 Matches
                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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CITY: I
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                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                  77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOV-97
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                                                                 GAATCGTCGGGGGTCAGGAGCCCCCAGGAGCAAGTGGCCCTGGCAGGTCAGCCTGAGAG 76
                 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
                                                 GCATCGTGGGAGGACATGAGGCCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 184
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02210-2211
                                                                                                                                Similarity
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linear
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MAST CELL PROTEASE THAT CLEAVES
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Pred. No. 8.1e-98;
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                                                                                                                 Mismatches 169;
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                                                                                                                                                                                                                                                                                                                              Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Steven
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield
                                                                                                                                                                                                                                                                                              APPLICANT: Stevens, TITLE OF INVENTION: TITLE OF INVENTION:
 PRIOR APPLICATION DATA:
                                                                                                                                                                                               STREET: 600 A
CITY: Boston
STATE: MA
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                                                                                  OPERATING SYSTEM: DOS
                                                                                SOFTWARE:
                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                 RY: U.S.A.
02210-2211
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                                                                                                                                                                                                                                600 Atlantic Avenue
                                                                              FastSEQ for Windows Version
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MAST CELL PROTEASE
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SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
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Local Similarity 76.48;
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                                                      TGCTGTGTGCCGGGAACACCCGGAGGGACTCCATGCCAGGGCGACTCCGGAGGGCCCCCTGG 613
                                                                                                                                                                                                                                                           ACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACA 553
                                                                                                                                                                                                                                                                                                                       TCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTG 493
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                                                                                                                 TGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGC 193
                                                                                                                                                                              TGCTGTGTGCTGGGAATGAAGGACATGACTCCTGCCAGGGCGACTCCGGAGGACCTCTGG
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ACTATGTCCCCAAGGACTTCTGA 848
                           ACTATGTCCCCAAAAAGCCGTGA 756
                                                                                    CCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACC 733
                                                                                                                                                                                                                                         ACTTGAAGTATCACAAAGGTCTCATCACAGGTGACAATGTCCACATTGTCCGAGATGACA 645
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Pred. No. 2.5e-96;
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/0 FILING DATE: 05-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chifu
 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                   17 GAATCGTCGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1103 base pairs TYPE: nucleic acid
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CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCC
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                                                                                                  TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCTGCCGGTCAGCAGGATCATCGTGC
                                                                                                                                                                   TCACTGCGGCACACTGTGTGGGACTGCACATCAAAAGCCCCAGAGCTCTTCCGTGTACAGC
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                                 ACCCCCACTACTACACAGTCGAGGATGGGGCAGACATTGCCCTGCTGGAGCTTGAGAACC
                                                               ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC
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Pred. No. 2.2e-92;
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                                                                                     CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGATGAGCGCCTCC 436
                                                                                                                                                                                                       ATGTCCCTCAGCGTTCCTGA 841
         ATGTCCCCAAAAAGCCGTGA 756
                                    AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCACT 736
                                                                                                                                                                           CCTCGGGGACTTCTTGCTGGGTAACAGGCTGGGGCGACATTGATAGTGACGAGCCTCTCC 521
                             AGGCCAATCGTCCTGGCATTTACACCCGGGTGACGTACTACCTGGACTGGATTCACCGCT 821
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Search completed: January 31, 2003, 05:25:27 Job time: 72 secs

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Title:
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Maximum DB seq length: 2000000000
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  676.2
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Match
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1 gggcccctcgagaa
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BQ720404 AGENCOURT
BQ082929 K-EST0144
BG542089 602571309
BQ721078 AGENCOURT
BI413250 602986390
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## ALIGNMENTS

FEATURES SOULCE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 BM919268 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS
Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12776 row: f column: 20 High quality sequence stop: 719. Location/Qualifiers 1. 1030	Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 1030) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs r@mail.nih.gov	BM919268 1 1030 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6715837 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748499 57, mRNA sequence. BM919268 BM919268 1 GI:19369647 EST.

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BASE COUNT
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  CTATGTCCCCAAAAAGCCGTGAGTCCANGGCC
                                       CTATGTCCCCAAAAAGCCGTGAAGCGGCCGCC
                                                                              CCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCA 734
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/clone_lib="NIH_MGC_120"
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/db_xref="taxon:9606"
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Pred. No. 6.9e-133;
0; Mismatches 39;
872
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Best Local Similarity
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                                                           TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
                                                                                               TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCCGGTCAGCAGGATCATCGTGC
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TGACCGCAGCGCACTGCGTGGGACC-----
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BQ720404.1
EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 904) (bases 1 to 904) (NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ720404 904 bp mRNA linea AGENCOURT_8477973 Lupski_sympathetic_trunk Homo IMAGE:6196776 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'-GACTAGTTCTAGATCGCGAGCGGCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor college of Medicine); available through Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
_Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:6196776"
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                                                                                                                                                                                                                                       Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 502)
Kim, N.S., Hahn, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ082929
K-EST0144841 S14K402
                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 59 row: B column: 11
High quality sequence stop: 502.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BQ082929
                                                                                                                                                                                                                        Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                     Genome Research Center
                                                                                                                                                                                                                                                                                                         Contact: Kim YS
                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                  Oh, K.J., Cheong, J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numan
                                                                                                                                                                                                                                                                                                                                   Frontier Korean
                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S14K402-59-B11"
/clone_lib="S14K402"
/cell_line="K402"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated wi
bacterial alkaline phosphatase (BAP) and then decapped
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E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                     EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOf' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Ecor I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcorI which site is also included in vector. An RNA strand
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99.2%;
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Pred. No. 8.3e-95;
0; Mismatches 4
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BG542089
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                                                                                                                                                DEFINITION
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                                                                                              mRNA sequence.
BG542089
BG542089.1 GI:
EST.
        Eukaryota; Metazoa; Chordata; C
Mammalla; Eutheria; Primates; C
1 (bases 1 to 736)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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602571309F1 NIH_MGC_77 Homo
Unpublished
                                                                      Homo sapiens
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Catarrhini;
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IMAGE:4695458 5',
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                                                                                                                                                                                                                                                                          CCACCGCCATTTCCTCTGAAGCAGG-TGAAGGTCCCCATAATGGAAAACCACATTTGTGA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATCGTTGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 172
                                                                                                                                             CGCAAAATACCACCTTGGCGCCT-ACACGGGAGACG-ACGTCCGCATCGTCCGTGACGAC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCC-GGGGATGCCGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGAAGGTCTCCAGCGTCCACACGGTCACCCTGCCCCCTGCCCTCAGAGACCTTCC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### TGACCGCAGCGCACTGCGTGGGACCGCGCCTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 292
                                      ATGCT - -
                                                                                                                                                                                                                                       CCACGGCATTTCCTTCTGAAGCAGGTTGAAGGTCCCCCATAATGGAAAACCACATTTGTGA 592
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                                                                                                       CGCAAAATAACACCTTGGGGCCTAACACGGGAGACGAAGGTCCGCATTCGTCCGGTGAAC
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/clone_lib="NIH_MGC_77"
/lab_host="DHIOB (TI phage-resistant)"
/lab_host="DHIOB (TI phage-resistant)
/lab_host="DHIO
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                                  --GTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCG--ACTCCGGAGG
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/db_xref="taxon:9606"
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Pred. No. 5.2e-89;
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ACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGG
                 ACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGG
                                                                       TGCTGGAGCTGGAGGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCCTGCCCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 917)
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National Institutes of Health,
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                                                                                                                                                                                                                                                                                                                 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

Technologies."

335 c 240 g 164 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Lupski_sympathetic_trunk"
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/clone="IMAGE:6189508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                           Score 444.4; DB 1
Pred. No. 6.4e-84;
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Best Local Similarity

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RESULT 6
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11351 row: c column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith
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National Institutes of Health, Mammalian
Unpublished (1999)
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602986390F1 NCI_CGAP_Lu33
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(bases 1 to 1000)
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                                                                                                                                                                                                                                                                                            quality sequence start: 32 quality sequence stop: 849. Location/Qualifiers
                                 Ph.D.
                                                                                                                                                     /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5142478"
/clone=lib="NCI_CGAP_LU33"
/clone=lib="NCI_CGAP_LU33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Notl; Site_2: ECORI; 1st
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/strain="CZECH II"
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3 Mus musculus cDNA clone
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Sciurognathi; Muridae;
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Eukaryota; Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarri 1 (bases 1 to 639)
Hillier, L., Lennon, G., Becker, M., Bor Chissoe, S., Dietrich, N., DuBuque, T., M., Hultman, M., Kucaba, T., Lacy, M.,
                                                                                                                                                                   AA131142
zl31b01.rl Soares_pregnant_uterus_NBHPU Homo sapiens
IMAGE:503497 5' similar to gb:M30038 ALPHA-TRYPTASE I
                                                                                                                       AA131142.1
EST.
                                                                                                                                                    (HUMAN);, mRNA sequence AA131142
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                                                                                                         human
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); Mismatches 163;
                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
 Bonaldo,M.F., Chiapelli,B.
[., Favello,A., Gish,W., Ha
M., Le,M., Le,N., Mardis,E.
                                                            Hominidae;
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                                                                                                                                                                                        CTACACGGGAGACGACCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCCG 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCAGCCG 60
                                                                                                     GAGAGCTTCATGCCAGGGCGACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTG
                                                                                                                                         GAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTG 635
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 CTACACCCGTGTCACCTACTTGG-ACTGGATCCACCACTATGTCCCCAAAAAGCCGT
                                 GCTACAGGCGGGCGTGGTCATCTGGGACGAGGGCTGTG-CAGTCCCAACCGGCCTGGCAT
                                                                                                                                                                        CTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACACCCCG
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                                                                     GCTGCAGGCGGGCGTGGTCAGCTGGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCAT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E. Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further insert Length: 894 Std Error: 0.00
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1 quality sequence stop: 349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_2: Eco RI; 1st strand cDNA was prime oligo(dT) primer [5' AACTGCAACAATAATTCCT.
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/clone="IMAGE:503497"
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/db_xref="GDB:3808485"
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   CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCC
                                    ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: James Cleaver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mamumalian
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/db_xref="taxon:9606"
/dlone="IMAGE:4803879"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NC /note="Sall; Cloned unidirectionally. Primer: Ol: Site_2: Sall; Cloned unidirectionally. Primer: Ol: Average insert size 1.5%b. Library constructed by Technologies. Note: this is a NCI_CGAP Library."
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Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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602503309F1 NIH_MGC_77
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Plate: LLCM1372 row: a column: 04
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
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/lab_bost="DHIUB (TI phage-resistant)"
/lab_bost="DHIUB (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR:LIB (Clontech); Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: graeme@helix.nih.gov
Plate: 01 row: h column: 02
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078
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sapiens cDNA clone bx01h02 5', mRNA sequence.
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/note-"Organ: Eye; Vector: pcMvSpORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pcWSpORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)15-3'
                                                                                                                                                                                                                                                             /tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
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JOURNAL COMMENT
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                                                                                                                                              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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BM991728
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                             mmalia; Eutheria; (bases 1 to 693)
                                                                                                                             primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                        Gene Index
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                 /db_xref="taxon:9606"
/clone="IMAGE:5870477"
/clone_lib="NCI_CGAP_DF1"
                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                           Location/Qualifiers
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93.5%;
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Pred. No. 2.6e-69;
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                                                                                                                                                                                                                                                                                                                                        Anatomy Project (CGAP),
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QΥ В Qy

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Qy В Qy В QΥ Вþ Qy

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DEFINITION
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                                                                                                                     REFERENCE
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                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        693 GGGTCACTGGCCTGGGCCATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 GGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357;
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                 BF850308
CM3-EN0077-181100-489-e06
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 376)
                                                                                                                                                                                     Homo sapiens
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/lab.host="DH10B (Life Technologies)"
/note="Organ: Bone; Vector: py773-Pac (Pharmacia) with a modified polylinker; Site_1: BCOR I; Site_2: Not I;
NCI_CGAP_DF1 is a normalized cONA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into py773-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_SEQ=GTTAAGCGTC"
179 c 241 g
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TAG_TISSUE=subchondral bone
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                                                                                                                                                                                                                                                       GI:12237470
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96.7%;
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Pred. No. 3.3e-64;
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BM989945 692 bp mRNA linear EST 17-JUN UI-H-DIO-ato-m-22-0-UI.sl NCI_CGAP_DIO Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0077-
181100-489-e06&t3=2000-11-18&t4=1)
Seq primer: puc 18 forward
Tick ben'itter:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt Simpson,A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: lung_normal; Vector: pucl8; Site_1: SmaI; Site_1: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue mRNA and cDNA amplification were performed under low stringency conditions."
115 c 121 g 78 t
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/clone_lib="EN0077"
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Pred. No. 4.1e-64;
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  635 GGCTGCAGGCGGGCGTGGTCAGCTGGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCA 694
                                             513
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nes 363; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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Tissue Procurement: Dr. Jose Mercuende
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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1 (bases 1 to 692)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_TISSUE=lung with fibrosis
TAG_SEQ=ATACGCGGTC"
182 c 242 g 137 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA
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/dev_stage="Adult"
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Pred. No. 6.5e-64;
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ACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAG 459
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Mammalia; Eutheria;
1 (bases 1 to 688)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE:5847122 3', mRNA sequence
                                                               Similarity
                                                                                                                                                   130
                                            Conservative
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                                                                                                                                                                                                                                                    adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                            constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing Not I site. Double stranded cDNA was ligated to an EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia)
with a modified polylinker; Site_1: Ecor I; Site_2: Not
NCI_CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
                                                                                                                                                   TAG_SEQ=ACACTTGCAC"
176 c 242 g
                                                                                                                                                                                                               ACACTTGCAC.
TAG_LIB=UI-H-EI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5847122"
                                                                                                                                                                                           TAG_TISSUE-chondrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Chondrosarcoma"
/dev_stage="Adult"
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97.3%;
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Primates;
                                       Score 348; DB Pred. No. 1.4e 0; Mismatches
                                         0;
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L.4e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                  High quality sequence start: 12 High quality sequence stop: 369
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Seg primer: puc 18 forward
                                                                                                                                                                                                                                                  Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0063
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                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0063"
/note="Organ: lung_tumor; Vector: pucl
Site_2: SmaI; A mini-library was made
                                              /dev_stage="Adult"
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Best Local Similarity 96.3
Matches 342; Conservative
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                                                                                                   311 GGGCGATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGAAGCAGGTGAAGGT
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                                                                CGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACC 702
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                                                                                                                                                                                                                                                                                                                                                                                                                           derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                             43.3%; Score 334.2; DB 12; Length 371; 96.3%; Pred. No. 9.8e-61; tive 0; Mismatches 13; Indels 0;
              2003, 06:50:06
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     987654321
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DNA encoding human
Human beta-tryptas
DNA encoding recom
DNA encoding human
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encoding
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24		24	20	24	24	24	24	24	24	24	24	24	21	21	19	19	24	24	21	21	21	21	21	21	21	21	21	19	19	19	19	24	24	24	24
AAS20790	S207	AAD23854	413	207	AAS20781	207	AAS20780	ABK35580	ABL66816	ABL62377	ABL61818	ABK64532	AAA34960	AAF21082	AAV42713	AAV44331	AAS20760	AAS20766	AAZ40172	AAA34962	AAF21084	AAA34956	AAF21078	AAA34955	AAF21077	AAA34957	AAF21079	AAV42711	AAV44329	AAV42712	AAV44330	AAS20787	2077	207	AAS20785
DNA encoding human		S	Human normal uteru	DNA encoding human	DNA encoding human	encoding	encoding	TPS2 di	C		Ď	Human benign prost	Human adenosine re	adenosi	cell	Human mast cell tr	encoding	DNA encoding recom	beta-trypt	Human adenosine re	Human low adenosin	Human adenosine re	S	nosine	w adenos	n adenosine	n low adenos	t cell	t cell	cell	Human mast cell tr	pr	encoding	ing	DNA encoding human

## ALIGNMENTS

RESULT 1 AAS20775

AAS20775;

AAS20775 standard; DNA; 771

ВP

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WPI; 2002-114578/15.
P-PSDB; AAU12009.
                                                                                                                                                                                                                                           09-APR-2002 (first entry)
DNA construct for producing enzymatically-inactive proteolytic
                                                                                                                                            WO200198470-A2
                                                                                                                                                                Synthetic.
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                            Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; mutant; ds.
                                                                                                                                                                                                                       DNA encoding human beta-II tryptase active site mutant H44A #1
                                                                  (PROM-) PROMEGA CORP
                                                                                     21-JUN-2000; 2000US-0598982.
                                                                                                        20-JUN-2001;
                                                                                                                           27-DEC-2001.
                                               Niles AL,
                                                                                                        2001WO-US19681.
                                               Haak-Frendscho
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The present invention relates to recombinant human proteolytic CC tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a CC proteolytic tryptase with an active site mutation (the construct drives capression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active cc beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the CC protease and its enzymatic activity, and for modelling studies. The CC cand in drug screening for compounds which act as tryptase inhibitors, CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant tryptase actives site mutants.
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                        CTGGAGCTGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
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GGAGGGCCCCTGGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGGGGTGGTCAGCTGG
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Db

Qy

GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGG

60

Matches

770;

Conservative

0;

Score 769.4; DB 24; Pred. No. 5.2e-148; 0; Mismatches 1;

Indels Length

0;

Gaps

0

Query Match Best Local Similarity

99.8**%**;

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RESULT 2
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ID AAS20783
ID AAS20783
ID O9-A
XX AAS2
XX AAS2
XX DNA
XX Huma
XX Huma
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XX WO20
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                                                                                     producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 104-105; 126pp; English.
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                                                               beta-II tryptase active site mutants
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      B₽;
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   147 A; 257 C;
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   243
   G; 124
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      T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolytic tryptase having
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RESULT 3
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                                                                                                         Beta-tryptase; human; DNA expression construct; protein production; combinatorial library screening; X ray crystallography; antigen;
                                                                                                                                                                                                   AAZ40175 standard; DNA;
15-MAY-1998;
                   29-OCT-1998;
                                       25-NOV-1999
                                                          WO9960139-A1
                                                                                                                                       Human beta-tryptase
                                                                                                                                                            18-FEB-2000
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                                                                             sapiens
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                                                                                                                                                                                                                                                               GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
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                                                                                                                                                           (first entry)
                   98WO-US22994.
                                                                                                                                       coding sequence
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CC This sequence encodes the human beta-tryptase. The invention relates to a CC DNA expression construct comprising (5' to 3') a promoter linked to a CC signal sequence which is linked to a sequence encoding human CC beta-tryptase. The DNA construct is useful for transforming host cells to CC express, post translationally process and secrete enzymatically active chuman tryptase with defined specifications. The transformant is useful for the production of large amounts CC of tryptase with defined specifications. The transformant is useful for CC pharmacological studies, combinatorial library screens and X ray CC crystallographic studies. The tryptase produced allows for the CC development of tryptase agonists and/or antagonists, is useful as an CC antigen to generate antihuman tryptase antibodies in various animals, CC can be used in screening for compounds which act as tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists cetc. may be useful as therapeutics. The tryptase does not require any CC post-expression or post-purification modifications or manipulations to initiate tryptase activity and it has enzymatic activity which compares CC favourably with cadaveric tryptase. The availability of enzymatically active tryptase facilitates the large scale screening of combinatorial CC libraries for specific tryptase. The tryptase can be used to detect low mast cell mediated diseases. The tryptase can be used to detect low cc levels of tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 43-44; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of enzymatically active
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Sequence 771 BP; 149 Α. 256 C; 242 G; 124 T; 0 other;

Matches Query Match Best Local Local Similarity Conservative 99.2%; 99.5%; 0 Score 764.6; DB Pred. No. 5e-147; Mismatches DB 21; 4; Indels Length 0; Gaps 0

1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG  $\vdash$ GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGG 60

밁 20

181 240

241 300 240

Вb

δÃ

В δÃ Вb Qy

241AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCCTGCCCCCT 360

421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAA 480

20 밁 δÃ DЪ δõ В δÃ

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RESULT 4
AAS2076
ID AAS25
XX AAS2
XX AAS2
XX DE DNA
XX Hume
KW enzy
XX Home
OS Synt
XX Key
FT CDS
FT
                                                                                                                                                                                                                  tryptase,
an active
  proteolytic tryptase with an
                           sequence
                                                                                                                                                                                                                                    DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase
                                                                                                                                                                                                                                                                                                                                                                                      Maffit M,
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                                                                     producing
                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROM-) PROMEGA CORF
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                                                                                                                    present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding
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DB; AAU12007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
is, active site mutants of these tryptases and the methods for gig these. The method involves the production of a DNA expression to comprising a promoter operably linked to a secretion signal which is operably linked to a DNA sequence encoding a tic tryptase with an active site mutation (the construct drives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                   Page
                                                                                                                                                                                                                  comprises DNA sequence site mutation -
                                                                                                                                                                                                                                                                                                                                                                                      Niles AL,
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                                                                                                                                                                   75-77;
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7..756
/*tag=_a
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/product= "Recombinant
/note= "This sequence |
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                                                                                                                    relates to recombinant human
                                                                                                                                                                 126pp;
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                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 771 BP; 149 A; 256 C;
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hes 767; Conserv
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CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACCGGTCACCCTGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                          AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC
                      GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
                                                                                                                                                                                                                     AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
                                                                                                                                                                                                                                                                                           CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
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99.5%;
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                                                                                                                                                                    The present invention relates to recombinant human proteolytic CC tryptases, active site mutants of these tryptases and the methods for CC producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a CC proteolytic tryptase with an active site mutation (the construct drives CC expression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the CC protease and its enzymatic activity, and for modelling studies. The CC enzymatically-active, recombinant proteolytic tryptase produced are CC useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, CC antagonists, agonists, etc. The present sequence encodes for human
                                                                                                                       Query Match
Best Local
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                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 72-74; 126pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation -
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                                                   sapiens
CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC
                                                                                                                                                                                            tryptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Beta-I tryptase"
/note= "This sequence lacks a start
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                                                                                                                                                                                                                                                                                                                                                                                                                                     proteolytic tryptase;
                                                                                                                                                                                                                                                                                                                                                                                                          mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                             2000US-0598982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-II tryptase active site mutant D91A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                     protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant beta-II tryptase;
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Maffit M,

Niles AL,

Haak-Frendscho

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to recombinant human proteolytic cryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies antigonists, agonists, etc. AAS20795-AAS20790 encode for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation - \,
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nes 765; Conserv
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                                                                                                                                                                                                                                                                      CTGGAGCTGGAGGCGGTGAAGGTCTCCAGCCACCGTCCACACGGTCACCCTGCCCCCT 360
                                                                                                                                                                                                                                                                                                                                   AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                   CACCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGCGACCGGACGTCAAGGATCTGGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGG
                GTCCGTGACGACATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGCGACTCC
                                                                                                                                                                                        CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC
GTCCGTGACGACATGCTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC
                                                                                          AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
                                                                                                                          CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                   GCCCTCAGGGTGCAACTGCGGGAGCAGCCTCTACTACCAGGACCAGCTGCTGCCGGTC
                                                                                                                                                         AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAA 480
                                                                                                                                                                                                                                                                                                                      AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGCAATCGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-II tryptase active site mutants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 761.4;
Pred. No. 2.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 242 G; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 24;
2.2e-146;
6;
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RESULT 7
AAS20784
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                        The present invention relates to recombinant human proteolytic CC tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal construct comprising a promoter operably linked to a secretion signal construct comprising a promoter operably linked to a secretion signal construct comprising a promoter operably linked to a secretion signal construct of a mature proteolytic tryptase mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity construct). The method is useful for producing enzymatically-active construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the corollar constructive, recombinant proteolytic tryptase produced are constructive, recombinant proteolytic tryptase produced are cuseful as an antigen to generate anti-human tryptase antibodies cand in drug screening for compounds which act as tryptase inhibitors, antiagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant constructives.
                                                                                                                                                                                                                                                                                                                                                                       DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation -
                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; proteolytic
enzyme; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2002
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DB; AAU12018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 107-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Niles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0598982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human beta-II tryptase active site mutant D91A #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haak-Frendscho
                                                                                                                                                                                                                                                                                                                                      126pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant beta-II tryptase;
                                                                                                                                                                                                                                                                                                                                                                                     tryptase
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Best Local Sir Matches 764; Query Match

Similarity

98.5%; 99.1%;

Conservative

0,

Score 759.8; DB 24 Pred. No. 4.7e-146; 0; Mismatches 7;

DB 24;

Length

0,

Gaps

0

Sequence

771

BP;

149 A; 257

C; 241 G; 124 T; 0 other;

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RESULT 8
AAS2077
ID AAS2
XX AAS2
AC AAS2
XX AAS2
XX BAS2
XX BA
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                                                       WO200198470-A2
                                                                                                      Synthetic
                                                                                                                                                                                Human; proteolytic enzyme; mutant; ds.
                                                                                                                                                                                                                                                       DNA encoding
                                                                                                                                                                                                                                                                                                            09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                              AAS20777 standard; DNA;
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                                                                                                                                                                                                                                                     human beta-II tryptase active site mutant S194A #1
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                                                                                                                                                                                                        tryptase;
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                                                                                                                                                                                                        protease; recombinant beta-II tryptase;
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CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC

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CTGGAGCTGGAGCAGCCGGTGAAGGTCTCCAGCCACACCACACGGTCACCCTGCCCCCT

CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT

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CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC

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                                                                                                                                                                                                    CC producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal cc sequence which is operably linked to a DNA sequence encoding a cc proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity cc due to the active site mutation, in hosts transformed to contain the cc construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide cc beta-II tryptase. The active site mutants of proteolytic tryptase provide cc a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The cc enzymatically-active, recombinant proteolytic tryptase produced are cc useful as an antigen to generate anti-human tryptase antibodies cand in drug screening for compounds which act as tryptase inhibitors, and candists, agonists, etc. AAS20775-AAS20790 encode for recombinant tryptase antibodies candiscipate the structural site mutants.
                                                                                      Matches
                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 88-90; 126pp; English.
                                                                                                                                                                     Sequence 771 BP; 150 A; 255 C; 241 G; 125 T; 0 other;
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Local 761;
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  GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGG
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                                                                                 Score 755; DB 24;
Pred. No. 4.5e-145;
0; Mismatches 10;
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           The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are
                                                                                                                                                                                                     Claim 7; Page 91-92; 126pp; English.
                                                                                                                                                                                                                                DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase an active site mutation - \,
                                                                                                                                                                                                                                                                                                                              Maffit M,
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Synthetic.
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; mutant; ds.
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 anti-human
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tryptase
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RESULT 10 AAS20785

AAS20785 standard;

DNA;

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09-APR-2002 DNA encoding

human

beta-II tryptase active

site mutant S194A

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(first entry)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 771 BP;
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                      GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
                                                        GCCGAGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCCGTGTCACCTACTTG
                                                                                             GTCCGTGACGACATGCTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGCGACTCC
                                                                                                                                                                                           CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
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                                               GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG
                                                                                                                                                                                                                    AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
                                                                                                                                                                                                                                           AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tryptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 A; 255 C; 241 G; 123 T; 0 other;
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 4.5e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to recombinant human proteolytic CC tryptases, active site mutants of these tryptases and the methods for CC producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a CC proteolytic tryptase with an active site mutation (the construct drives CC expression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the CC enzymatically-active, recombinant proteolytic tryptase produced are CC enzymatically-active, recombinant proteolytic tryptase antiodies. The CC enzymatically-active, recombinant proteolytic tryptase inhibitors, and in drug screening for compounds which act as tryptase inhibitors, thuman tryptase antiodies. AAS2075-AAS20790 encode for recombinant tryptase inhibitors, thuman tryptase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonists, agonists, etc. AAS201/13 AND401/human beta-II tryptase active site mutants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 110-111; 126pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maffit M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 771
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es 760; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       construct for producing enzymatically-inactive proteolytic ptase, comprises DNA sequence encoding proteolytic tryptase having
                                                                                                                                                                                                 CACCCCAGTGGGTGCTGACCGCCGCGGGGGTGCGTGGGACCGGACGTCAAGGATCTGGCC
                                                                                                                                                                                                                                                     CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC
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CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGGTCACACGCTCACCCTGCCCCT
                                                                                                                                    GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC
                                                                                                                                                                                   CACCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC
                                                                                                                                                                                                                                                                   CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC
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                                                                                 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
                                                                                                                  GCCCTCAGGGTGCAACTGCGGGAGCAGCCTCTACTACCAGGACCAGCTGCTGCCGGTC
                                                  AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
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98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 C;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 753.4; DB
Pred. No. 9.6e-14
0; Mismatches 1
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.6e-145;
.es 11; Indels 0;
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RESULT 11
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                                                                                                Claim 7;
                                                                                                                                            DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase
                                                                                                                                                                                                                                             Maffit M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytic tryptase;
                                                                                                                                                                                                AAU12020
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                                                                                             Page 113-114; 126pp; English.
                                                                                                                               site mutation
                                                                                                                                                                                                                                             Niles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
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                                                                                                                                sequence encoding
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tryptases, active site mutants of these tryptases and the methods for producting these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a

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Best Local Similarity
Matches 760; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic tryptase with an active site mutation (the construct drives
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               GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
                                                                                GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCCGTGTCACCTACTTG
                                                                                                                                                                                                                  GTCCGTGACGACATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGCGACTCC
                                                                                                                                                                                                                                                                                   AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
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                                                                                                                                                  GTCCGTGACGACATGCTGTGCCGGGAACACCCCGGAGGGACTCATGCCAAGGAGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGAGCTGGAGGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
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                                                                                                                                                                                                                                                                    AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGGAGACGACGTCCGCATC
                                                                                                                                                                                                                                                                                                                                                     AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
                                                                 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG
                                                                                                                                 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 152 A; 256 C; 240 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.7%;
98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC tryptases, active site mutants of these tryptases and the methods for CC producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a CC proteolytic tryptase with an active site mutation (the construct drives CC expression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide CC a tool to investigate the structural and functional properties of the CC protease and its enzymatic activity, and for modelling studies. The companies of the consymatically-active, recombinant proteolytic tryptase produced are CC useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant contains the mutants.
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200198470-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROM-) PROMEGA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to recombinant human proteolytic
  CGGGAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC
                                                                                      ACCGCCGCGCGTGCGTGCGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
                                                                                                                                                                                                                           CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG
                                                                                                                                                                                                                                                                                                            ATCGTCGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC
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; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 94-95; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 139 A; 245 C; 231 G; 120 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human beta-II tryptase active site mutant H44A #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase
                                                                            P-PSDB;
                                                                                                                                                                                                                                                        21-JUN-2000; 2000US-0598982
                                                                                                                                                                                                                                                                                                          20-JUN-2001; 2001WO-US19681
                                                                                                                                                                                                                                                                                                                                                            27-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding human beta-II tryptase active site mutant H44A #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-2002
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                                                                                                                                                                                                        (PROM-) PROMEGA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCCCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACAGTTCTACACCGCCCAGATCGGAGCGGACCATCGCCCTGCTGGAGCTGGAGGAGCCG 318
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DB; AAU12021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC tryptases, active site mutants of these tryptases and the methods for CC producing these. The method involves the production of a DNA expression CC construct comprising a promoter operably linked to a secretion signal CC sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives CC expression of a mature proteolytic tryptase that lacks enzymatic activity CC due to the active site mutation, in hosts transformed to contain the CC construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide CC beta-II tryptase. The active site mutants of proteolytic tryptase provide CC a tool to investigate the structural and functional properties of the CC enzymatically-active, recombinant proteolytic tryptase produced are cuseful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, againsts, etc. AAS20775-AAS20790 encode for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to recombinant human proteolytic ptases, active site mutants of these tryptases and the methods for
                    AAGGTGAATGGCACCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG
                                                                                                                                                                                                                                    CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
                                                                                                                                                                                                                                                                                       CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGCCGCGCGTGCGTGCGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
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                                                                                                        TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
                                                                                                                                            AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG
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                                                                                                                                                                                                                 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
                                                                                                                                                                                                                                                                                                                          CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA
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 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG
                                                                       TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         735 BP; 139 A; 246 C; 230 G; 120 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 115-117; 126pp;
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99.9%;
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Pred. No. 1.1e-140;
0; Mismatches 1;
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ARESULT 14
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                                                                                                                                                                                                                                                             This nucleotide sequence includes a coding region for human comparison to the invention provides:

Compositions comprising an isolated tryptase-7 that may include chimeric proteins that contain (a) a human tryptase for all but the active site region and (b) the substrate-binding pocket of mouse tryptase-7 or its homologues (see AAW6423-39); a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product, to decrease codes for a tryptase-7, or an expression product, to decrease (SP); and a method of producing a mature SP by expressing the inactive zymogen in a host cell, and cleaving the enterokinase consciptibility domain. The tryptase-7 polypeptides can be used to treat disorders mediated by undesirable thrombus clot formation such as myocardial infarction and reocclusion following angioplasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7; blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy; ss.
                                                                                          Sequence
                                                                                                                                                thrombosis, cerebral embolism, renal vein and peripheral arterial thrombosis. They are also useful for all surgical procedures tha require decreased blood clots.
                                                                                                                                                                                                                                 such as myocardial infarction and reoccursion totalogues of blood clots associated with pulmonary thromboembolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 66; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compositions containing tryptase-7, e.g. mouse mast cell protease-7 - are used to treat clot formation in e.g. myocardial infarction, reccclusion following angioplasty or pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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/*tag= a
                                                                                       190 A; 409 C;
94.8%;
98.7%;
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Score 731; DB 19;
Pred. No. 3.6e-140;
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                                                                                          other;
                            Length 1128;
                                                                                                                                                                                                                                              deep vein
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Query Match

Best Local Similarity

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RESULT 15
AAV42712
ID AAV42
XX AAV42
XX AAV42
XX AAV42
XX Human
DE Human
XX Mast
KW Mast
KW Trypt
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antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
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                     ATGTCCCCAAAAAGCCGTGAAGCGGCC
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## ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX347853	RESULT 1
Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same	Maffit, M., Niles, A.L. and Haak-Frendscho, M.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX347853.1 GI:18495660	AX347853	Sequence 20 from Patent WO0198470.	AX347853 771 bp DNA linear PAT 01-FEB-2002		

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Finkaryota; Metazoa;
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/db_xref="GI:18495677"
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ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
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Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
Enzymatically-active recombinant human .beta.-
of making same
Patent: US 6274366-7
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/db_xref="G1:18495649"
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EPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENH
ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
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/db_xref="taxon:9606"
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Location/Qualifiers
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/protein_id="AD22417.1"
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/db_xref="G1:18495646"
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EPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENH
                                                        /note="unnamed
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/db_xref="taxon:9606"
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/db_xref="GI:18495663"
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         CTGGAGCTGGAGCCGGTGAAGGTCTCCAGCCACCGTCCACACGGTCACCCTGCCCCCT
                                                                                                       AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
                                                                                                                                                               GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC
                                                                                                                                                                                       CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC
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                                                                                                                                         GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCCGGTC
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/db_xref="G1:18495679"
/translation="LEKRIVGGEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTARHCVGFDVKDLAALRVQLREGHLYYQDQLLPVSRIIVHPQFYTAQIGAAIALLELE EPVNYSSHVHTVYLPPASETFEPGMPCWVTGWGDVDNDERLPPFFLKOVKVFIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAAPNRPGIYTRVTYYLDWIHHYVPKKP"
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                                           CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC 120
                                                                                           GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGG
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            CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC
                                                                                GGGCCCCTCGAGAAAAGAATCGTCGGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGG
                                  CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC
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Sequence 24
AX347857
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                                                                                                                                                                                     /protein_id="CAD22422.1"
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/tds_xref="GI:18495655"
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ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRDSCQGDAGGPLVCKVNGTWLQAGVVSW
GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
a 255 c 241 g 125 t
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<7. .756
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Craniata; Ve Catarrhini;
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Mammalia; Eutheria; I
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WO 0198470-A 40 27-DEC-2001;
CORPORATION (US)
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SWGEGCAQPURPGIYTRDTYXLDWIHHYVPKKP"
240 g 125 t
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Eutheria;
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Primates;
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ACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCTCAGGGTGCAACTG
            ACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
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Sequence
AX347861
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nilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                         /note="unnamed
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KYHLGAYTTGDDVRIVRDDMLCAANTRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGC
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M33492.1 GI:339982
serine protease; tryptase-II.
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TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT
                                                                                                                                  CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG
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Vanderslice, P., Ballinger, S.M., Tam, E.K., Craik, c.S. and Caughey, G.H.

Human mast cell tryptase: multiple cDNAs multigene serine protease family

Proc. Natl. Acad. Sci. U.S.A. 87 (10), 38
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Draft entry and computer-readable sequence for Sci. U.S.A. (1990) In press] kindly submitted by P. Vanderslice, 02-APR-1990.
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/db_xref="01:339983"
/rtans!ation="LULLLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQ
/trans!ation="LULLLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQ
VSLRVHGPYMMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYYQDQLLP
VSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPFGMPCWVTGWG
DVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDS
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/db_xref="taxon:9606"
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Search completed: January 31, 2003, 06:12:33 Job time: 2817 secs

